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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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151.5	159.5	159.5	172.5	197.5	197.5	202	226.5	236	251.5	255	255	256.5	269.5	289	290	290	299	299	310.5	348	354	423	445	451	457.5	461	483	537.5	w	556	568	575.5	595
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AAY36089	AAG91332	AAB76843	AAM24336	AAU37141	AAU34281	AAB96555	ABG10933	ABB52506	AAU35119	AAM23744	AAM23715	AAY40903	ABG10934	AAY40907	ABG29884	AAU01581	AAB90591	AAB90590	AAM24062	AAU01608	AAU01607	AAU02884	AAY40906	AAU02883	AAR44143	AAW11325	ABB58504	AAB90637	AAB90555	AAY44016	AAY44017	ABB65651	AAB29621
Extended human sec	C glutamicum prote	Corynebacterium gl	Drosophila EST enc	Staphylococcus aur	Staphylococcus aur	Putative P. abyssi	Novel human d‰agno		Enterococcus faeca	Human EST encoded	Human EST encoded	Arabidopsis thalia		Arabidopsis thalia	Novel human diagno	Human secreted pro		Human secreted pro	Human EST encoded	Human secreted pro	Gene #21 human sec	$\vdash$		Human HsNHE-6 poly	Rabbit sodium ion/	Human Na+/H+ excha	Drosophila melanog		Human secreted pro	Schizosaccharomyce	Saccharomyces cere	8	Cat flea HMT Na/H

## ALIGNMENTS

RESULT 1
AAB573251
AC AAB5
XX AAB5
XX AAB6
AC AAB6
XX Vacu
DT 14->
XX Vacu
XX Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in WPI; 2001-191648/19. N-PSDB; AAF75752. Iida S, 24-AUG-1999; 24-AUG-2000; 2000WO-JP05722. 01-MAR-2001. WO200114560-A1 Vacuole pH regulation; morning glory; flower colour. Protein regulating the pH of vacuoles 14-MAY-2001 AAB73251; AAB73251 standard; Protein; 542 horticulture (SUNR ) SUNTORY LTD. Ipomoea nil. Tanaka S, (first entry) 99JP-0236800. Inagaki Ŗ

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RESULT 2
AAB12786
ID AAB1
XX AAB1
AC AAB1
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Best Local :
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            JP2000157287-A.
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                                 Atliplex gmelini
                                                                  Atliplex
                                                                                        Atliplex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVF
                                                                                                                                                                                                                                                                                               PLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMIT
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                                                                                                                                                                                                                                                       ESDMITGPEVARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
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                                                       x gmelini;
H+ antipor
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                                                                                       gmelini
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                                                       antiporter
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                                                                                    Na+ and H+ antiporter protein.
                                                                 Na
                                                                                                                                                        Protein;
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                                                   plus and H plus antiporter protein; r protein; transformed plant; high s
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Pred. No. 4.8e-270;
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RESULT 3
AAB73253
ID AAB7
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AC AAB7
XX

AAB73253 standard;

Protein;

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Best Local Sim
Matches 418;
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
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542
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                                                                                                                                                                                VTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSES
                                                                                                         HSEATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPL
                                                                                                                                                                                                                                                                                         LSSLLQN--SDLFTSDHASYVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGLCTG
                 SPVEQS
                                   DVGNGNHEDTTEPRTIVRPSSLRMLLNAPTHTVHHYWRKFDDSFMRPVFGGRGFVPFVPG
                                                                                                                                                                                                                                                      STIISLGALSIFKKLDIGTLELADYLAIGAIFAATDSVCTLQVLNQDETPLLYSLVFGE
SPTEQS
                                                     DMITGPE-----
                                                                       ISVVLFSTMVFGLLTKPLIMFLLPQPKHFT--
                                                                                                                                                                                                                                                                SCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGE
                                                                                                                                             HAFATLSFVAEVFLFLYVGMDALDIEKWRFVSDSPGISVAVSSILLGLVMVGRAAFVFPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 10-12;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                     -VARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAG
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76.6%;
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                                                                                                                                                                                                                                                                                                                                                                  50;
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Pred. No. 1.8e-205;
0; Mismatches 65;
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                                                FPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMI
                                                                                TTKHTFATLSFIAEIFIFLYVGMDALDIEKWKFVSDSPGTSIKVSSILLGLVLVGRGAFV
                                                                                                                                                                           FGEGVVNDATSVVLFNAVQNFDLSHISTGKALQLIGNFLYLFASSTFLGVAVGLLSAFII
                                                                                                                                                                                    FGEGVVNDATSVVLFNAIQSEDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYII
                                    FPLSFLSNLTKKNPEDKISFNQQVTIWWAGLMRGAVSMALAYNQFTRGGHTQLRANAIMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable
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                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a sodium ion and rice origin for production of
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N-PSDB; AAA61876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB11832 standard;
                                                                                                                                                                                                                                                                                                                                                            Claim 1a; Fig 1; 43pp; Japanese.
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LLVESEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGAVKIF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPLSFLSNLTKKTPEAKISFNQQVTIWWAGLMRGAVSMALAYNQFTRGGHTQLRANAIMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFV
                                                                                                                   401;
                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanaka Y;
                                                                                                                                                                                             535
                                                                                                                   Conservative
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                                                                                                               74.3%; Score 2055.5; DB 2
76.4%; Pred. No. 3.2e-198;
tive 49; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                   proton counter-transporter protein salt tolerant rice transformants
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                                                                                                                                                    21; Length
                                                                                                                 Indels
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                                                                                                                                                                                                                                                                 (BLUM/)
                                   Claim 36; Fig 1A; 93pp;
                                                                        Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants
                                                                                                                                  WPI; 1999-571840/48.
N-PSDB; AAZ22591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sodium; proton; antiport; transporter; salt tolerance; salt management; transgenic plant; survival; soil; farming; accumulation; irrigation;.
 The invention relates to an isolated nucleic acid molecule encoding
                                                                                                                                                                                         Blumwald E,
                                                                                                                                                                                                                                                                                                                         18-MAR-1998;
15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY40901;
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                                                                                                                                                                                                                                (AHAR/)
                                                                                                                                                                                                                                                 (SNED/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTKPLIRLLLP-----ASGHP--VTSEPSSPKSLHSPLLTSMQGSDLESTT--NIVRPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMTTGPEVARPTA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMLMAYLSYMLAELLDLSGILTVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFIAETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHLDIDFILDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEGVVNDATSVVLFN
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                                                                                                                                                                                                                              SNEDDEN W. AHARON G.
                                                                                                                                                                                                                                                                                    BLUMWALD E.
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99US-0116111.
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                                      English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                         14-MAY-2001
Vacuole pH regulation; flower
                          Protein regulating the pH of vacuoles
                                                                                                                AAB73254 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242
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                                                                                                                                                                                                                                                                                                                                                                                    FLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTV
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; Pred. No. 9.3e-197;
57; Mismatches 71;
  colour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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Best Local S
Matches 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a protein, which has vacuolar pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give ne breeds of colorful plants for cut flowers, particularly applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            applicable in horticulture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 57-60; 68pp; Japanese
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DB; AAF75766.
                                                                                                                                                                                                                                                                                                                                                 LATGVIILLISGGKSSHLLVFSEDLFFIYALPPIIFNAGFQVKKKSFFRNFATIMMFGAV
                                                                                                                                                                                                                                                                                                                                                              LCTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAI 118
                                                                                                                                                                                                                                                             VFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYI
                                                                                                                                                                                                                                                                                                                GTLISCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSL
                                                                                                                                                                                                                                                                                                                                                                                                   GFESVIKLAASETDNLWSSGHGSVVAITLFVTLLCTCIVIGHLLEENRWMNESIIALIIG
                                                                                                                                              GTLISFIIISLGTIAFFPKMNMR-LGVGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSL
            DSESDMIT------GPEVARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVP
                                                                                                             VFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIM
                                                                                                                                                                                                                                                 VFGEGVVNDATSVVLFNAVQNFDLPHMSTAKAFELVGNFFYLFATSTVLGVLTGLLSAYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                    389;
DSVAELFSIRGQTSQGGEPVARPSSLRMLLTKPTHTVHYYWRKFDNAFMRPVFGGRGFVP
                                                 ITSTITIVLESTVVFGLMTKPLINLLIPSPKLNRS-----VSSEPLTPNSITIPLLGESQ
                                                             || ITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQP
                                                                                                VFPLSFLSNLAKKSPLEKISLRQQIIIWWAGLMRGAVSMALAYKQFTREGLTVERENAIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUNTORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 70.5
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0236800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.6%;
70.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1953.5; DB 2
Pred. No. 6.4e-188;
6; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                           358
                                                                                                                                                                                                                           298
                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                           178
                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                           478
                                                                                                    420
                                                                                                                                                  360
                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                    180
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RESULT 8
AAX440905
ID AAX4
AC AAX4
XX AAX4
XX Sodi
CO ATAL
XX Sodi
KW Sodi
KW Crop
OS Aral
XX Aral
XX Aral
XX Aral
XX Aral
AC CR
PF 18-1
PF 18-2
PF 18-2
PF 18-3
PF 18
       δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QY
                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to a transporter from Arabidopsis thaliana. The Na/H transporter polypeptides provide a means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
       . 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants - \,
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                        atriplex,
                                                                                                                                                                                                                                                                                                                                                             strawberries, spinach,
                                                                                                                                                                                                                                                                                                                                                                                             crops,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 50; Fig 5A-B; 93pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blumwald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-1998;
15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09947679-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY40905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY40905 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AHAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (APSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BLUM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2000
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                                                          N
VILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLIS
                                                                            LSSLLQN-SDLFTSDHASVVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGLCTGV
                                                                                                                                                                                                                                                                                                                                                                                                                  in India,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1999-571840/48
                                                  LDSLVSKLPSLSTSDHASVVALNLFVALLCACIVLGHLLEENRWMNESITALLIGLGTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVAGSPVEQSPR 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVPGSPTERSVR 547
                                                                                                                                                                                                                                                                                                                                                  n India, Australia, and prairies in USA or Canada. Commer
such as potatoes, tomatoes, brassica, cotton, sunflower,
erries, spinach, lettuce, rice, soybean, corn, wheat, rye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNEDDEN W. AHARON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APSE
                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLUMWALD E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ22595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proton; antiport; transporter; salt tolerance; salt management;
nic plant; survival; soil; farming; accumulation; irrigation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                                                                                                                                                                             sorghum,
                                                                                                                                                                                                                                                              547
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apse M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                             tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0078474.
99US-0116111.
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                                                                                                                                                                                                                                                                                                                                alfalfa, salicornia and others would benefit from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                              67.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Snedden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                         54;
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                                                                                                                                                    Score 1867; DB 20;
Pred. No. 3.3e-179;
4; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     farming; accumulation; irrigation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G;
                                                                                                                                                    Indels
                                                                                                                                                                                                   Length 547;
                                                                                                                                                    14;
                                                                                                                                              Gaps
  123
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RESULT 9
AAU02882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                    10-NOV-1999;
18-AUG-2000;
22-AUG-2000;
                                                     Transgenic plants with salt tolerance, drought and freeze and increased yield and flower size comprise exogenous H+
                                                                                                              Gaiola
                                                                                       WPI; 2001-328862/34.
                                                                                                                                                                                                                                                                                                        freeze tolerance; 35S promoter; sodium; calcium; manganese; saline soil; thale-cress.
                                                                                                                                                                                                                                                                                                                           AtNHX1; tonoplast pyrophosphatase hydrogen ion translocating pump; AV vacuolar pyrophosphatase; salt tolerance; drought tolerance; cation;
                                                                                                                                  (WYCO-) UNIV CONNECTICUT (WHED ) WHITEHEAD INST.
                                                                                                                                                                                                                10-NOV-2000; 2000WO-US30955
                                                                                                                                                                                                                                      17-MAY-2001
                                                                                                                                                                                                                                                             WO200133945-A1
                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana AtNHX1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                           AAU02882;
                                                                                                                                                                                                                                                                                                                                                                                                                                AAU02882 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        472 FIEPSGNHNVPRPDSIRGFLTRPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESDMITGPEVARPTALRMLLRTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTT---SEPSSPKHFTVPLLDNQPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNDATSVVVFNAIQSFDLTHLNHEAAFHLLGNFLYLFLLSTLLGAATGLISAYVIKKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVCLFSTVVFGMLTKPLISYLLP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLSNLAKKNQSEKINFNMQVVIWWSGLMRGAVSMALAYNKFTRAGHTDVRGNAIMITSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFATLSFLAETFIFLYVGMDALDIDKWRSVSDTPGTSIAVSSILMGLVMVGRAAFVFPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTIISLGVTQFFKKLDIGTFDLGDYLAIGAIFAATDSVCTLQVLNQDETPLLYSLVFGEG
                                                                                                              RA;
                                                                                                                                                                   99US-0164808.
2000US-0226223.
2000US-0644039.
                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
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                                                    resistance
genes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480
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                                                                                                                                                                                                                                                                                                                                        AVP1;
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The sequence represents an Arabidopsis thaliana AtNHX1 polypeptide which

Example 1; Fig 6; 68pp; English

increased

vacuolar pyrophosphatase

expression

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RESULT 10
AAY40902
ID AAY40
XX
AC AAY40
XX
AC AAY40
XX
XX
DT 18-JA
XX
XX
XX
KW Sodiu
KW trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is a tonoplast pyrophosphatase hydrogen ion (H+) translocating pump. Transgenic plants can be made by transforming plant cells with exogenous tonoplast pyrophosphate driven H+ pump genes and an exogenous nucleic acid encoding a protein, such as AVP1, which alters expression of vacuolar pyrophosphatase. Salt tolerance may be introduced into a plant via transformation of the cells to induce upregulation of vacuolar phosphatase expression. Drought and/or freeze tolerance may also be introduced through transformation with DNA encoding a vacuolar H+ translocating pump linked to a promoter such as the 35S promoter. These processes are useful for bioremediating soil and removing cations such as support plant growth. Plants which grow in saline soil can be produced and yield and flower size of plants can be increased.
      Sodium; proton;
transgenic plan
                    Sodium;
                                            Arabidopsis thaliana Na/H transporter AtNHX2.
                                                                              18-JAN-2000
                                                                                                                                      AAY40902 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 YILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LSSLLQN-SDLFTSDHASVVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGLCTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                              P 532
                                                                                                                                                                                                                                          P 541
                                                                                                                                                                                                                                                                 FIEPSCHHNVPRPDSIRGFLTRPTRTVHYYWRQFDDSFMRPVFCCRGFVPFVPGSPTERN
                                                                                                                                                                                                                                                                                                                                                                                                                                           ESDMITGPEVARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
                                                                                                                                                                                                                                                                                                                          TVCLFSTVVFGMLTKPLISYLLP------HQNATTSMLSDDNTPKSIHIPLLDQ--DS
                                                                                                                                                                                                                                                                                                                                              TVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTT---
                                                                                                                                                                                                                                                                                                                                                                                   FLSNLAKKNQSRKINFNMQVVIWWSGLMRCAVSMALAYNKFTRAGHTDVRGNAIMITSTI
                                                                                                                                                                                                                                                                                                                                                                                                    FLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVNDATSVVVFNAIQSFDLTHLNHRAAFHLLCNFLYLFLLSTLLGAATCLISAYVIKKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TILLISKGKSSHLLVFSEDLFPIYLLPPIIPNACFQVKKKQFFHNFVTINLPCAVGTIIS
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 >ton; antiport; transporter; salt
plant; survival; soil; farming;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   571 AA;
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                                                                           (first
                                                                         entry)
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 salt tolerance; sa
ing; accumulation;
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               salt management;
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Matches Best

310;

Conservative

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Mismatches

120;

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TGVVILLLSGGKSSHLLVESEDLEFIYLLPPIIFNAGFQVKKKQFEVNFMTIMLFGAIGT 120

SGTVILLISKGKSSHILVFDEELFFIYLLPPIIFNAGFQVKKKKFFHNFLTIMSFGVIGV 118

Local

Similarity

299 301

TRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVF

TLYFGRHSTTRELAIMVLMAYLSYMLAELFSLSGILTVFFCGVLMSHYASYNVTESSRIT KLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVT 300 GEGVVNDATSVVLFNAVQKIQFESLTGWTALQVFGNFLYLFSTSTLLGIGVGLITSFVLK

298

SRHVFAMLSFIAETFIFLYVGTDALDFTKWKTSSLSFGGTLGVSGVITALVLLGRAAFVF

239 241 179

181

GEGVVNDATSVVLENAIQSEDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIK 240

238

178

LISCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVF 180

119

121

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Query Match
                                                                  The Na/H transporter polypeptides provide a means of intracellular sait management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high sait levels that would normally inhibit growth of the crop species this would be useful in farming land in areas that are generally considered unproductive through sait accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley atriplex, sorghum, alfalfa, salicornia and others would benefit from increased sait tolerance.
                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to the AtNHX2 transporter from Arabidopsis thalians.
                                            Sequence
                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-571840/48
N-PSDB; AAZ22592.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Blumwald E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-1998;
15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BLUM/) BLUMWALD E.
(APSE/) APSE M.
(SNED/) SNEDDEN W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                         36;
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AHARON G.
                                                                                                                                                                                                                                                                                                                       Fig 1B;
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99US-0116111
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                                                                                                                                                                                                                                                                                                                     93pp;
57.8%; Score 1599.5; DB 20; 58.7%; Pred. No. 2.9e-152;
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                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB59364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB59364 standard;
                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide
                                                                                                                         (ABB57737-ABB72072)
                                                                                                                                                                                                                        Disclosure; SEQ ID NO 4884; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL03467.
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                                                                   Sequence
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  SSLLQNSDLFTS-----DHASVVSMNLFVALLCACIVLGHLLEEN--RWVNESITALIIG 58
                                                                                                                                                                                                                                                                                                                          JC,
                        Similarity 33...
59; Conservative
                                                                   649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmental biology;
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                                                                                                                                                                                                                                                                                                                                                                  2000US-191637P
2000US-0614150
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Pred.
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                         Mismatches
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No. 2.
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                        Gaps
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STLVTDPPLIDSHAVEQEHNSSLSLFFVICVIMLGILLIHSMLQTGFQYLPESIVVVFLG

constructs, recombinant viruses nucleic acids of the invention, antibodies against the proteins,

encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the protein antibodies against the proteins, a method of identifying inhibitors of the proteins.

The invention relates to novel cat flea (Ctenocephalides felis) nucleiclds which are expressed in hindgut and Malpighian tubule (HMT) tiacids which are expressed in hindgut and Malpighian tubule (HMT) tissue. The invention also relates to

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RESULT 12
AAB29621
ID AAB29
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Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea
                                                                                                                                                                                                                                                                                                  Ctenocephalides
                                                                                                                                                                                                                                                                                                                                Cat flea; hindgut and Malpighian tubule protein; flea infestation; vaccine; antiparasitic; therap
                                                                                                                                                                                                                                                                                                                                                                Cat flea
                                                                                                                                                                                                                                                                                                                                                                                                      AAB29621;
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                                                                                                                                                                                                                                                                                                                       diagnosis; detection.
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                                                                                Claim 10; Page 891-893; 964pp; English.
                                                                                                                                              N-PSDB;
                                                                                                                                                                            Brandt KS,
                                                                                                                                                                                                                    09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LCTGVVILLLSG--GKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFG
                                                                                                                                             2000-656323/63.
DB; AAC95370, AAC95371, AAC95372,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLI 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWH
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                                                                                                                                                                                               HESKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the proteins, and compositions comprising the inhibitors for administration to an animal. The nucleic acids, and the proteins they cencode may be used in the prevention, treatment and diagnosis of diseases cassociated with flea infestations. For example, the nucleic acids may be used to produce an HMT or HNC protein according to standard recombinant CDNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein The HMT and HNC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and culturing the proteins and their role in metabolism. The HMT and HNC proteins may be used as antigens in the production of specific antiodies, and in assays to identify modulators (agonists and cativity. The antibodies and antibodies and antibodies and antibodies and antibodies and activity. The antibodies may also be used to used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The present sequence represents a cat flea HMT protein of the invention.
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Best Local Similarity
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                  ABB65651
                                                ABB65651 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                            555 LDHKYLRPFFTRR 567
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                                                                                                                                                                                                              TRRQQKAITLSKTREWGSAIDSELLSELTTEEE
                                                                                                                                                                                                                                                                                                      GHTSLH-----ENAIMITSTVTVVLFSTVVFGLMTKPLINLLLFPHKQMPSGHSSMTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSLLQNSDLFTSDHASV-----VSMNLFVAL--LCACIVLGHLLEEN--RWVNESITALI 56
                                                                                                                                                                              -DDSFMRPVFGGR 526
                                                                                                                                                                                                                                              EPSSPKHETVPLL~--DNQPDSE--SDMITGPEVARPTALRMLLRTPTHTVHRYWRKF--
                                                                                                                                                                                                                                                                                    ---SLHLEFSDETRHVIITTTLIIVLCTTLIFGGATMPLLKFL----
                                                                                                                                                                                                                                                                                                                                                     --LCLIGRAANIFPLSWLVNQFREH---KITKKMAFIMWFSGL-RGAISYAL-----
                                                                                                                                                                                                                                                                                                                                                                                         VGLILVGRAAFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTS
                                                                                                                                                                                                                                                                                                                                                                                                                               YTHFNLSTVTQITMQQTMRTLAFIAETCVFAYLGMAIFSF----RHRVEPALVIWSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVVFALISALLLKHVDLRKYPS-LELGMMLVFTYAPYVLAEGIHLSGIMAILFCGIVMSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPVLNMLVFGESILNDAISIVLTTAVLESNNPLMTTAEAVVSGLN----RFCLMFFASAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPLLYSLVFGEGVVNDATSVVLFNAIQSFD---MTSFDPKI-GLHFIGNFLYLFLSSTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFAIFGTAISAFVVGAG-VYLLGMADVAYNLSFVESFAFGSLISAVDPVATVAIFHALDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGALIGLIINLMSSKNIANWKNEEAFSPTAFFLVLLPPIIFESGYNLHKGNFFONIGSIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           809
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%; Pred. No. 6.6e-51;
114; Mismatches 190
                                                727 AA
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                                                                                                                                                                                                            -RDVTFTQVRRGLEFIR
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Best Local :
                                                                                                                                                                                                                                                                                                                                            Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                        (ABB57737-ABB72072). The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 23745; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                       178
                                                                                                                                          121
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                                                                                                                           LISCSIIS---FGAVKIF-KHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPL-L 175
                                                                                                                                                                                                                                                                                                          LSSLIQNSDLFTSDHASVVSMNLFVALLCACIVIGHLLEENR--WVNESITALIIGLCTG 62
MIGAAMGCLTA-LMTKFTRVRDFPLLESALFVLMSYSTFLLAEATELTGVVAVLFCGICQ 410
                 FLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVM 285
                                                                        YSLVFGEGVVNDATSVVLFNAIQS------
                                                                                                                                                                                                                           AIIRY--AGTSATLVHMQVEPQGVPTYSDKLPPDTLWFRYPVNQTNGTKPPEGIKTYAYV 177
                                                                                                                                                                                                                                                                                  LNHRIQSLDLL------VEVFLLALTVLTIWLFKHHRVSWLHETGLAVIYGLIVG 119
                                                      YALVLGESVLNDAVAIVLSGAIQNYGEHYSNTGEFETTAF-
                                                                                                            TLSAFLIGGEMYGCVKLMPKYLSSSF-TFLDSLYFGALISPTDPLTILAIFNDLRVDVNL
                                                                                                                                                                   FRGQVHDVDENEIDLKATFDPEVFFNIILPPIIFYAGYSLKKKYFFRNLGAILTFAIVGT 237
                                                                                                                                                                                   Similarity
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2000US-0614150.
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a and
                                                                                                                                                                                                                                                                                                                                        20.8%; Score 575.5; DB 2
28.8%; Pred. No. 7.9e-49;
tive 99; Mismatches 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                           Mismatches 196;
                                                                     ---FDMTSFDPKIGLHFIGNFLYLFLSST 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                    22;
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                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                         145;
                                                                                                                                                                                                                                                                                                                                                                     727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BLUM/) BLUMWALD E.
(APSE/) APSE M.
(SNED/) SNEDDEN W.
(AHAR/) AHARON G.
                                                                                a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to an Na/H antiport transporter from the budding yeast Saccharomyces cerevisiae. The Na/H transporter polypeptides provide a means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules encoding useful in genetic engineering sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae Na/H
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                                poor irrigation, e.g. in India, Aus
Commercial crops, such as potatoes,
                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule encoding
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 8B; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blumwald E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1998;
15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGYLQDVEGGGVNRNKMRLSGGTDTNLDTPVDGTNGSLGGASGGR-----
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     strawberries,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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99US-0116111
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t; survival;
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     spinach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transporter; salt tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiport transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LDNQPDSESDMITGPEVARPTALRMLLRTPTH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sodium/proton transport polypeptides,
alt tolerance in crop plants -
                                Australia, and prairies in USA or Canada oes, tomatoes, brassica, cotton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
     lettuce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aharon
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     rice,
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     soybean,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     salt management;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              irrigation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RRNSHEK
        corn, wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505
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RESULT 15
AAY44016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rye, barley, atriplex, sorghum, alfalfa, salicornia benefit from increased salt tolerance.
                         WO9947679-A2
                                                Schizosaccharomyces
                                                                                                  Sodium;
                                                                                                                         Schizosaccharomyces pombe Na/H antiport transporter.
                                                                                                                                                  18-JAN-2000
                                                                                                                                                                           AAY44016;
                                                                                                                                                                                                   AAY44016
                                                                                    transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                    441
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                                                                                                                                                                                                                                                                                                                AVSSNKNLPNNISTTGGNTFGGLNETENTSPNPARSSMDKRNLRDKLGTIFNSDSQWFQN 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGVLIGILVALLLKHTHIRRY-PQIESCLILLIAYESYFFSNGCHMSGIVSLLFCGITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLSILIFAIPGTFISAVVIGI-ILYIWTFLGLESIDISFADAMSVGATLSATDPVTILSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLPSPDLPGSDDPIAGDPDVDLNPVTEEMFSSWALFIMLLLLISALWSSYYLTQKRIRAV 89
                                                                                                                                                                                                                                                                                          FDDSFMRPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSQDET-PLLYSLVFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSST 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FMTIMLFGAIGTLISCSIISFGAVKIFKHLDIDFLD--FGDYLAIGAIFAATDSVCTLQV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HETVLSIFYGMVIGLIIRMSPGHYIQDTVTFNSSYFFNVLLPPIILNSGYELNQVNFFNN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLQNSDLFTSDHASV----VSMN-----LFVALLCACIVLG---HLLEEN-RWV
                                                                                                                                                                                                                                                                  FDEQVLKPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                            MRGAVSIALAYN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILVGLILVGRAAFVFPLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHYAYYNMSRRSQITIKYIFQLLARLSENFIFIYLGLELFTEVELVY----KPLLIIVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNAYKVDPKLYTIIFGESLLNDAISIVMFETCQKFHGQPATFSSVFEGAGLFLMTFSVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NESITALIIGLCTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVN 108
                                                                                                                                                                                                                                                                                                                                                                  IKTGCISEEDTSDDEFDIEAPRAINLLNGSSIQTDLGPYSD------NNSPDISIDQF
                                                                                                                                                                                                                                                                                                                                                                                                                    -RGAVGVALALGIQGEYKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I---SICVARWCAVFPLSQFVNWIYRVKTIRSMSGITGENISVPDEIPYNYQMMTFWAGL
                                                                                   proton; antiport; transporter;
nic plant; survival; soil; farmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 27.2 56; Conservative
                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                  509
                                                                                                                                                                                                                                                                                          523
                                                pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            -KFTTSGHTSLHENAIMITSTVTVVLFSTVVFGLMTKPLINLL-
                                                                                                                                                                                                                                                                                                                                                                                         LPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMI 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117;
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Pred.
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                                                                                                                                                                                                                                                                                                                                            TGPEVARPTALRMLLRTPTHTV----HRYWRK
                                                                                     farming; accumulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -FLSNLAKKNSS--DKISFRQQIIIWWAGL
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                                                                                                  salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
3.7e-48;
nes 203;
                                                                                                  tolerance;
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                                                                                                  salt management;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124;
                                                                                       irrigation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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23-SEP-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule encoding CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment CC and capable of increasing salt tolerance in a cell. This sequence CC corresponds to an Na/H antiport transporter from the fission yeast CC schizosaccharomyces pombe. The Na/H transporter polypeptides provide CC a means of intracellular salt management, particularly in plants. The CC sequences are useful for producing transgenic plants that are capable CC of surviving in soil with high salt levels that would normally inhibit CC growth of the crop species. This would be useful in farming land in areas CC that are generally considered unproductive through salt accumulation and CC commercial crops, such as potatoes, tomatoes, brassica, cotton, CC sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, CC rye, barley, atriplex, sorghum, alfalfa, salicornia and others would cC benefit from increased salt tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid molecules encoding sodium/proton transport polypeptides useful in genetic engineering salt tolerance in crop plants - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAR-1998;
15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 8A; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-571840/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AHAR/) AHARON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BLUM/) BLUMWALD E.
(APSE/) APSE M.
(SNED/) SNEDDEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1999;
                                                                                                                                                                                                                                                                                                     209
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  422
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                                                                                                                                                                                      307
                                                                                                                                                                                                                            263
                                                                                                                                                                                                                                                              247
                                    418 MITSTVTVVLFSTVVFGLMTKPLINLL---------LPPHKQMPS---GHSS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 SMNLFVALLCACIVLGHLL------EENRWVNESITALIIGLCTGVVILLLSGGKSSHL 76
                                                                                                                                                  VLAQLSENFIFIYLGMSLFTQVDLVYKPIFILIT---TVAVTA-----SRYMNVFPL 370
                                                                                                                                                                                                                PS-IESCIILLMAYTSYFFSNGCHMSGVVSLLFCGITLKHYAFFNMSYKAKLSTKYVFR 321
                                                                                                                                                                                                                                                                                                                                                                           SFLNFENLSMTFVEALSMGATLSATDPVTVLAIFNSYKVDQKLYTIIFGESTLNDAVAIV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSFHSTYFFNVLLPPIILNSGYELHQSNFFRNIGTILTFAFAGTFISA--VTLGVLVYIF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVESEDLEFIYLLPPIIFNAGFQVKKKQFFVNEMTIMLFGAIGTLISCSIISFGA-VKIF 135
                                                                                                                                                                                                                                                                                                                                     LFNAIQSFDMTSFDPKIGLHF-----IGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGR 246
                                                                                                                                                                                                                                                                                                                                                                                                               KHLDIDFLD--FGDYLAIGAIFAATDSVCTLQVL-SQDETPLLYSLVFGEGVVNDATSVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWALFILLV----LLIGALLTSYYVQSKKIRAIHETVISVFVGMVVGLIIRVSPGLIIQNM
LRATTLYVVVLTLIIFGGTTARMLEILHIETGVAADVDSDTEIGMLPWQQSPEFDLENSA
                                                                                                                                                                        TLSFVAETFIFLYVGMDALD----IEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPL 362
                                                                                                                                                                                                                                                            HSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFA 306
                                                                                            SFLSNLAKK----NSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENA-I 417
                                                                                                                                                                                                                                                                                                 MFETLQQFQGKT-----LHFFTLFSGIGIFIITFFISLLIGVSIGLITALLLKYSYLRR
                                                                        SNLLNKFHRQRNGNLIDHIPYSYQMMLFWAGL-RGAVGVALA-----AGFEG--ENAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.1%; Score 556; DB 20; illarity 28.9%; Pred. No. 5.1e-47; Conservative 119; Mismatches 181;
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99US-0116111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aharon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
  481
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                                                                          421
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Search completed: October 18, 2002, 12:25:19 Job time: 38 secs

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Maximum

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Total number of hits satisfying chosen parameters:
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Perfect score:
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score grea
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R;Dante M.; Wamsley, P.; Gibson, A.
submitted to the EMBL Data Library, June 1997
submitted to the EMBL Data Library and 1997
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A;Reference number: Z14440
A;Accession: T01804
A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 1-457 < DAN>
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Na+/H+-exchanging	conserved hypothet	probable Na+/H+ an	probable Na+/H+ an	probable sodium/hy	sodium/proton exch	Na+/H+ antiporter	Na+/H+ antiporter	probable Na+/H+ an	probable Na+/H+ an	probable Na+/H+ an	Na+/H+ antiporter	hypothetical prote	hypothetical prote	probable Na+/H+ an	protein F20B17.4 [

## ALIGNMENTS

TM021B04

#text\_change 22-Oct-1999 Arabidopsis thaliana

A; Experimental source: cultivar Columbia C; Genetics: A; Introns: 55/3; 95/2; 128/1; 148/1; 163/3; 240/3; 256/2; 286/3; 320/2; 400/3; 421/3 A;Cross-references: EMBL:AF007271; NID:g2191181; PID:g2191184; GSPDB:GN00063; ATSP:A\_ 64 VILLLSGKKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLIS 123 VMSHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAV VVNDATSVVVFNATQSFDLTHLNHEAAFHLLGNFLYLFLLSTLLGAAVSPLFSSLPFFLT CSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEG GLLCAYIIKKLYFG------RHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGI CTIISLGVTQFFKKLDIGTFDLGDYLAIGAIFAATDSVCTLQVLNQDETPLLYSLVFGEG GLISAYVIKKLYFGRWPHINCHRHSTDREVALMMLMAYLSYMLAELFDLSGILTVFFCGI LDSLYSKLPSLSTSDHASVVALNLFVALLCACIVLGHLLEENRWNNESITALLIGLGTGV VMSHYTWHNVTESSRITTKHTFATLSFLAETFIFLYVGMDALDIDKWRSVSDTPGTSIAV 44; Score 1732.5; DB 2; Pred. No. 2.4e-123; 4; Mismatches 46; Indels Length 457; 21; Gaps 241 181 61 63 361 301 231 183 ω

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-703 <WILL-
A;Cross-references: EMBL:AL034393; PIDN:CAA22320.1; CESP:Y18D10A.6
A;Experimental source: clone Y18D10A
C;Genetics:
A;Gene: CESP:Y18D10A.6
A;Introns: 23/3; 56/1; 103/2; 246/3; 352/3; 492/2; 578/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Y18D10A.6 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C:Accession: T26529 R:Harris, B.
RESULT 3
$66734

R; Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A; Reference number: $69534

A; Accession; $69734
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A; Accession: T26529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLLPPIIFENAYNLNKGYFFSNFVPILTFAIFGTTISAMVIGAG-LYILGAIGLIFEFTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFVALLCACIVLGHLLEENRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDLFFI 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYIPYGFAEALDLSGIMAILFCGISMSQFTRHNVSPIAQITFRHTFRTISFVAETSTFAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FNSLPASEIITSAFV-TFTEMFFFSACLGVGIGLLSALLFKHVDL-RKTPSLEFALLLIF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FECFAFAAMISAVDPVGTLAIFQAVKVESLLYMLVFGESMLNDAVSIVLAATALRHAKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDYLAIGAIFAATDSVCTLQVLSQDET-PLLYSLVFGEGVVNDATSVVLF-----NAIQS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFVIMLATLVVHMLIVSKIHWMPESLAIVALGALIG-SILSYSRRDWSEIEALSPDVFFL 196
                                                                                                                                                                                                                                          LPFISFINRCYPNERQRKRRRTPRNKESTGNSSALMMSKTQEMSFF
                                                                                                                                                                                                                                                                                                                 SMKNQIIMWFSG-MRGAVCFALVLYM-----DLDKEKKSILLTTVLFLILFTTIFLGGSA
                                                                                                                                                                                                                                                                                                                                                SERQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGLMT 437
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; Pred. No. 6.8e-37;
78; Mismatches 181; Indels
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A; Molecule type: DNA
A; Residues: 1-633 <DIE>
A; Cross-references: EMBI
C; Genetics:
A;Molecule type: DNA
A;Residues: 1-569 <MUR>
A;Ross-references: EMBL:Z97208; PIDN:CAB10103.1; GSPDB:GN00066; SPDB:SPAC15A10.06
A;Experimental source: strain 972h-; cosmid c15A10
C;Genetics:
                                                                                                                                                 probable sodium/hydrogen exchanger - fission yeast C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 C;Accession: T37706 R;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.;
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A;Map position: 4R
C;Superfamily: hypothetical protein yvgP
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A;Reference number: Z21738
A;Accession: T37706
A;Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLPSPDLpGSDDPIAGDPDVDLNPVTEEMFSSWALFIMLLLLISALWSSYYLTQKRIRAV
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                                                                                                                                                                                                                                                                                                          FDEQVLKPVF
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                                                                                                                                                                                                                                                                                                                                            FDDSFMRPVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                              IKTGCISEEDTSDDEFDIEAPRAINLLNGSSIQTDLGPYSD-----NNSPDISIDQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RGAVGVALALGIQGEYKFT----
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                                                                                                                                                                                                                                                                                                            609
                                                                                                                                       : Wood, V.;
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27.2%;
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Pred. No. 3
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                                                                                                                                         June
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                                                                                      GB/EMBL/DDBC
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                                                                                                                                                          Rajandream,
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                                                                                                                                                                                                                           (Schizosaccharomyces
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A;Cross-references: EMBL:Z69646; PIDN:CAA93476.1; GSPDB:GN00028; CESP:F57C7.2
A;Experimental source: clone F57C7
C:Genetics:
                                                                             A;Gene: CESP:F57C7.2
A;Map position: X
A;Introns: 33/3; 81/1
                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-629 <WIL>
                                                                                                                                                                                                                         A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                   submitted to the EMBL Data A; Reference number: 219625 A; Accession: T22848
                                                                                                                                                                                                                                                                                                                             hypothetical protein F57C7.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T22848
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A:Map position: 1
A:Introns: 11/1; 116/3; 356/3
C:Superfamily: hypothetical protein yvgp
                                                                                                                                                                                                                                                                                                               R; White,
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     Local Similarity les 158; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 SMNLFVALLCACIVLGHLL-----EENRWVNESITALIIGLCTGVVILLLSGGKSSHL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRDDQAQWLTRFDEEVIKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MITSTVTVVLFSTVVFGLMTKPLINLL---------LPPHKQMPS---GHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHLDIDFLD--FGDYLAIGAIFAATDSVCTLQVL-SQDETPLLYSLVFGEGVVNDATSVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFLSNLAKK----NSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENA-I 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLAQLSENFIFIYLGMSLFTQVDLVYKPIFILIT---TVAVTA-----SRYMNVFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFLNFENLSMTFVEALSMGATLSATDPVTVLAIFNSYKVDQKLYTIIFGESILNDAVAIV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSFHSTYFFNVLLPPIILNSGYELHQSNFFRNIGTILTFAFAGTFISA--VTLGVLVYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGA-VKIF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWALFILLV----LLIGALLTSYYVQSKKIRAIHETVISVFVGMVVGLIIRVSPGLIIQNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTHTVHRYWRKFDDSFMRPV 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MELSDASAEPVVVDQQFTTEHFDEGNIAPTLSKKVSS----TFEQYQRAAGAFNQFFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTTSEPS-----SPKHF----TVPLLDNQPDSESDMITGPEVARPT-ALRMLLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNLLNKFHRQRNGNLIDHIPYSYQMMLFWAGL-RGAVGVALA----AGFEG--ENAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLSFVAETFIFLYVGMDALD----IEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPS-IESCIILLMAYTSYFFSNGCHMSGVVSLLFCGITLKHYAFFNMSYKAKLSTKYVFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFNAIQSFDMTSFDPKIGLHF-----IGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRATTLVVVVLTLIIFGGTTARMLEILHIETGVAADVDSDTEIGMLPWQQSPEFDLENSA
                                                                         81/1; 119/2; 155/3; 207/2; 239/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                           #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                 20.0%;
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                                                                                                                                                                                                                                                                                       Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119;
     77;
 Score 552.5; DB 2;
Pred. No. 5.3e-34;
77; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 556; DB 2;
Pred. No. 2.5e-34;
9; Mismatches 181
                                                                                                                                                                                                                                                                                     February
                                                                         274/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                   Length 629;
 Indels
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53;
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                                                                     354/1; 386/3; 421/3;
Gaps
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16;
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                                                                                                                                                                                                                                               A; Note:
A; Note:
                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L11236; NID:g205318; PIDN:AAA72350.1; PID:g205319 R;Collins, J.F.; Honda, T.; Knobel, S.; Bulus, N.M.; Conary, J.; DuBois, Proc. Natl. Acad. Sci. U.S.A. 90, 3938-3942, 1993 A;Title: Molecular cloning, sequencing, tissue distribution, and function A;Reference number: A47449; MUID:93248205
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A;Molecule type: mRNA
A;Residues: 1-813 <WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Wang, Z.; Orlowski, J.; Shull, G.E. J. Biol. Chem. 268, 11925-11928, 193 JA; Title: Primary structure and functional A; Reference number: A46748; MUID:93280160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Na+/H+ exchanging protein NHE-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change
C;Accession: A46748; A47449
                                                                                                                                                                                                                                                                                                     A; Molecule type: nucleic acid
A; Residues: 117-813 <COL>
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                                                                                                                                                                                                                                                                                 A; Experimental source: intestine
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                                                                                                                                                                                 Query Match
Best Local Similarity
                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441
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                                                     70
                                                                                         71
                                                                                                                           14 LFTSDHASV---VSMNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLS
                                                                                                                                                                                                                                         sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:130778, NCBIP:130779)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
             GVDEKSPPAMKTDVFFLYLLPPIVLDAGYFMPTRPFFENLGTIFWYAVVGTLWNSIGIGL
                                               GGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTL----ISC
                                                                                       VFTLDYPHVQIPFEITLWILLASLAKIGFHLYHKLPTIVPESCLLIMVGLLLGGIIF--- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSTV-VFGLMTKPLINLLLPPH-KQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMI 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRRR---PKIPKRYQHMILFAGL-RGAMAFALA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVL 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVTVLVNGGLTSWMIDYLQIKHGKDAIEEGQRLENSMSSSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIMESFIFCYIGVSV-----FVTNNQRWS--FSFLLFSLISITASRALFVYPLSWLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LESSLFVLISYISFLVAEVCGLTGIVSVLFCGIAQAHYTYNNLSDESQSNTKHFFHMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGPEVARPTALRMLLRTPTHTVHRYWRKFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FNAIQSFDMTSFDPKIGLHFIGN----FLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPL-LYSLVFGEGVVNDATSVVL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILV--GRAAFVFPLSFLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEVIENFSTSS--EAITLODFGSAIAGFAGVFFGSLMLGFMIGCMNAFLTKMTLISEHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTSIFQMGYSFKELLFFGALISATDPVTIISVFNDMNVEADLFALIFGESALNDAVAIVL
                                                                                                                                                                   Conservative
                                                                                                                                                                                     17.5%;
28.0%;
                                                                                                                                                                 86;
                                                                                                                                                               Score 485.5; 1
Pred. No. 8.3e
86; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of a novel gastrointestinal isof
                                                                                                                                                                 es 215;
                                                                                                                                                                                                       DB 2;
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05-Nov-1999

538

489

440 367 309

249 272

330

79;

Gaps 69

18;

functional expression

70 .

Ghishan,

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Na+/H+-exchanging protein NHE-2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C;Accession: A46747
C;Accession: A46747
R;Tse, C.M.; Levine, S.A.; Yun, C.H.; Montrose, M.H.; Little, P.J.; Pouyssegur, J.; Donc J. Biol. Cchem. 268, 11917-11924, 1993
A;Title: Cloning and expression of a rabbit cDNA encoding a serum-activated ethylisoprop A;Peference number: A46747; MUID:93280159
A;Accession: A46747
A;Scatus: preliminary
A;Scatus: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-809 <TSE>
A;Experimental source: ileal villus cells
A;Rote: sequence extracted from NCBI backbone (NCBIN:133350, NCBIP:133351)
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                                           300 TTRHSFATLSFVAETFIFLYVGMDALDIE---KWKFVKNSQGLSVAVSSILVGLILVGRA 356
                                                                                                                                                                                                                                                                                                                                                                                70
                                                                                                                                                                                                                                                                                                                                                                                                                         70
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 LFTSDHASV---VSMNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 17.4%; Score 482.5; DB 2; Local Similarity 27.8%; Pred. No. 1.4e-28;
                                                                                                                                                                    KKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVNDATSVVLENAIQSE----DMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYII 239
TIKYFMKMLSSVSETLIFIFMGVSTVGKNHEWNWAFV------CFTLAFCLIWRA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWR----KFDDSFMR 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGVFVLTQVINWFR---TIPLTFKDQFIIAYGGL-RGAICFALVF----LLPATVFPRKK 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTRHSFATLSFVAETFIFLYVGMDALDIE---KWKFVKNSQGLSVAVSSILVGLILVGRA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ-DETPLLYSLVFGEG 183
                                                                                      R---FTHNIRVIEPLFVFLYSYLSYITAEMFHLSGIMAITACAMTMNKYVEENVSQKSYT 357
                                                                                                                             KKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRV 299
                                                                                                                                                                                                                                                       SLFGICQIEAFGLSDITLL---QNLLFGSLISAVDPVAVLAVFENIHVNEQLYILVFGES 243
                                                                                                                                                                                                                                                                                            SIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ-DETPLLYSLVFGEG 183
                                                                                                                                                                                                                                                                                                                                                                                                                       VFTLDYPHVQIPFEITLWILLASLAKIGFHLYHKLPTIVPESCLLIMVGLLLGGIIF--- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIKYFMKMLSSVSETLIFIFMGVSTVGKNHEWNWAFV------CFTLAFCLIWRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R---FTHNIRVIEPLFVFLYSYLSYITAEMFHLSGIMAITACAMTMNKYVEENVSQKSYT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LINDAVTVVLYNLFKSFCQMKTIQTVDVFAG---IANFFVVGIGGVLIGILLGFIAAFTT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLFGICQIEAFGLSDITLL---QNLLFGSLISAVDPVAVLAVFENIHVNEQLYILVFGES
                                                                                                                                                                                                                                                                                                                                       GVDEKSPPAMKTDVFFLYLLPPIVLDAGYFMPTRPFFENLGTIFWYAVVGTLWNSIGIGV 186
                                                                                                                                                                                                                                                                                                                                                                              GGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTL-----ISC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GHWGHNFWRDKFKKFDDKYLR 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 809;
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	DISGQIGHNYLRDKWANFDRRF	492	Db	
	MITGPEVARPTALRMLLRTPTHTVHRYWRKEDDSEM 519	484	Qy	
	IVVFFTVIFQGLTIKPLVQWLKVKRSEHREPKLNEKLHGRAFDHILSAIE 491	442	Db	
	TVVLESTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESD 483	424	Qy	
	LDG	394	Db	
	TTSGHTSLHENAIMIT	368	Qy	
	SGAETIIFWFLGISAVDPLIWTWNTAFVLLTLLFVSVFRAIGVVLQTWLLN 393	343	Db	
	FVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPL	310	Qy	
	VIEPGFVFIISYLSYLTSEMLSLSSILAITFCGICCQKVVKANISEQSATTVRXYMKMLA	283	Db 2	
	DREVALMMINGVI.SVITAAELEVI.SGILTVFECGIVMSHVITWHVVTESSRVTTRHSEATIS	٥ ٦	2	
	LYNVFQSFVTLGGDKVTGVDCVKGIVSFFVVSLGGTLVGVVFAFLLSLVTRFTKHVR	226	DB 49	
	: H	169	⊋ Db	
	KHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ-DETPLLYSLVFGEGVVNDATSVV 192	136	Qy	
	LIPTVFFFYLLPPIVLDAGYFMPNRLFFSNLGSILLYAVVGTVWNAATTGLSLYGVFLSG 168	109	망	
	-SEDLFEIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGAVKIF 135	80	Qy	
	IIALWVLVASLAKIVFHLSHKVTSVVPESALLIVLGLVLGGIVLAADHIASFT 108	56	DЬ	
		22	Qy	
19;	17.0%; Score 471.5; DB 2; Length 832; al Similarity 28.5%; Pred. No. 9.8e-28; 148; Conservative 92; Mismatches 197; Indels 83; Gaps	Query Ma Best Loo Matches	Z III O	
	;Accession: A40205; ;Accession: A40205; ;Status: preliminary ;Molecule type: mRNA ;Residues: 1-832 <-TSE> ;Cross-references: GB:M87007; NID:g165548; PIDN:AAA31420.1; PID:g165549 ;Keywords: transmembrane protein	ccessi tatus: lolecul lesidue ross-r	C A A A A A A A A A A A A A A A A A A A	
kidney-sp	J. Biol. Chem. 267, 9340-9346, 1992 J. Biol. Chem. 267, 9340-9346, 1992 A.FIILLE: Cloning and sequencing of a rabbit cDNA encoding an intestinal and a new force of the control of the con	Biol. itle:	э. Д. Б.Т.	
	on: A40205 M.; Brant, S.R.; Walker, M.S.; Pouyssegur, J.; Donowitz, M.	se, C.	R; 1	
	ESULT 8 40205 la+/H-exchanging protein 3 - rabbit la+/H-exchanging protein 3 - rabbit l;Alternate names: Na+/H+ antiporter l;Alternate names: Na+/H+ antiporter l;Species: Oryctolagus cuniculus (domestic rabbit) l;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999	A40205 Na+/H+-excha N; Alternate C; Species: O C; Date: 28-A	RESULT A4 0205 Na+/H++ Na+/H++ C; Spec: C; Date	
	VKTGIEDVCGHWGHNFWRDKFKKFDDKYLR 539		Дb	
	ப	477	Qγ	
	IMITSTYTVYLESTYVEGLMEKELINLELEPHNQMESGHSSMITSESSENGIVELLUM 4/0 :   : :  : :  :  :  :   EFITAAIVVIEETVEILGITIRPLYEEFLDVKRSNKKQQAVSEEHCREFDH 509	459	Db	
		40/		
	AFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKETTSGHTSLHENA 416       :   : : : : : :	357	γ <sub>2</sub>	

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CAMP-activated Na+/H+-exchanging protein betaNHE - rainbow trout C; Species: Oncorhynchus mykies (rainbow trout) C; Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997 C; Accession: A46188 R; Borgese, F; Sardet, C:; Cappadoro, M.; Pouyssegur, J.; Motais, R. Proc. Natl. Acad. Sci. U.S.A. 89, 6765-6769, 1992 A; Title: Cloning and expression of a cAMP-activated Na+/H+ exchanger: evident A; Reference number: A46188; MUID:92357712 A; Accession: A46188 A58tatus; preliminary; not compared with conceptual translation A; Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
B407204
Na+/H+-exchanging protein 3 - rat
N;Alternate names: Na+/H+ antiporter
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C;Accession: B40204
R;Orlowski, J; Kandasamy, R.A.; Shull, G.E.
J. Biol. Chem. 267, 9331-9339, 1992
A;Title: Molecular cloning of putative members of the Na/H exchanger gene f;
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A;Cross-references: GB:M85300; NID:g205706; PIDN:AAA41702.1; C;Keywords: transmembrane protein
                                                                                                                                                                                                                      A46188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 146; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IIEPGFVFVISYLSYLTSEMLSLSAILAITFCGICCQKYVKANISEQSATTVRYTMKMLA
                                                                                                                                                                                                                                                                                                                                                                               VIFQGLTIKPLVQWL-----
                                                                                                                                                                                                                                                                                                                                                                                                              TVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPK------HFTVPLLDNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGAETIIFMFLGISAVDPVIWTW------NTAFVLLTLVFISVYRAIGVVLQTWILNRY
                                                                                                                                                                                                                                                                                                                                    DSESDMITGPEVARPTALRMLLRTPTHTVHRY----WRKFDDSFMRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RMYQLETI----DQVVMSYGGL-RGAVAYALV----VLLDEKKVKEKNLFVSTTLIVVFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYNVFESFVTLGGDAVTGVDCVKGIVSFFVVSLGGTLVGVIFAFLLSLVTR---FTKHVR
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Pred. No. 1.6e
89; Mismatches
                                                                                                                                                                                                                                                                                                -QIGHNYLRDKWSNFDRKFLSKV
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A;Gene: NHE1
C;Keywords: glycoprotein; :
F;76,374,414/Binding site:
                                                                                                                                                                                                                      C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C:Accession: S30198; S29541
R:Counillon, L.; Pouyssegur, J.
Biochim. Biophys. Acta 1172, 343-345, 1993
A:Title: Nucleotide sequence of the Chinese hamster Na(+)/H(+)
A:Reference number: S30198; MUID:93192332
                                                                                                                                                                                                                                                                                                          Na+/H+-exchanging protein - Chinese hamster
N;Alternate names: Na+/H+ antiporter; Na+/H+ exchanger
C;Species: Cricetulus griseus (Chinese hamster)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                                                                                                                                   A;Cross-references: EMBL:X68970; NID:g49472; C;Genetics:
                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-822 <CO
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A;Experimental source: cephalic kidney hematopoietic tissues
A;Note: sequence extracted from NCBI backbone (NCBIP:113525)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GVCGHYGHYHWKEKLNRFNKTYVKRWLIAGENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQSFD----MTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFVQGMTIRPLVELLAVKKKK------ESKPSINEEIHTEFLDH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -KFRIVKLTKKDQFIVAYGGL-RGAIAFSLGY--LLSNSHQMRN---LFLTAIITVIFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETLIFIFLGVSTVAGPHAWNWTFV-----ITTVI--LCLVSRVLGVIGLTFIIN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETFIFLYVGMDAL---DIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEEFSKVGTVTVLDVFLG----VVCFFVVSLGGVLVGAIYGFLAAFTSR----FTSHTRVIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPPIILDAGYFLPIRPFTENVGTILVFAVIGTLWNAFFMGGLLYALCQIESVG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLIS------CSIISFGAVKIFKH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLALLMKLGFHLIPRLSAVVPESCLLIVVGLLVGGLIKVI--GEEPPVL--DSQLFFLCL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148;
                      Similarity
                                                                                                                                                                                                          S30198
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                                                                                                                                                                      <C0U>
                   16.9%; Score 467.5; DB 28.2%; Pred. No. 1.9e-27
                                                                      ion transport; membrane protein
carbohydrate (Asn) (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100;
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                                                                                                                                                 PIDN:CAA48771.1;
                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184;
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                                      Length
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                                                                        #status predicted
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   71;
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Gaps
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P Qy

109

25 MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL 83

ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGG--LIKGVGETPPFL--QSDV

Eri

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C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 28-May-1999
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 28-May-1999
C;Date: 08-Feb-1996 #sequence.revision 08-Feb-1996 #text_change 28-May-1999
C;Accession: A57644
R;Ghishan, F.K.; Knobel, S.M.; Summar, M.
Genomics 30, 25-30, 1995
A;Title: Molecular cloning, sequencing, chromosomal localization, and tissue dis
A;Title: Molecular cloning, sequencing, chromosomal localization, and tissue dis
A;Accession: A57644
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-698 cgHI>
A;Cross-references: GB:S81591; NID:g1478393; PIDN:AAB36180.1; PID:g1478394
C;Genetics:
A;Gene: GDB:SLC9A2
A;Cross-references: GDB:132596; OMIM:600530
A;Map position: 2g11.2-2g11.2
C;Keywords: transmembrane protein
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A57644
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Best Local
p
172 LIGILLGFIAAFTTR---FTHNIRVIEPLFVFLYSYLSYITAEMFHLSGIMAITACAMTM 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 SDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVF 433
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                                                  226 FLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVM 285
                                                                                             115 HVNEQLYILVFGESLLNDAVTVVLYNLFKSFCQMKTIQTVDVFAG---IANFFVVGIGGV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 TALRMLLRTPTHTVHRYWR----KFDDSFMR 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                    56 IIGLCTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLF 115 ::|| | :| | | | | :
                                                                                                                                                                                                                                                                                                                                             Local Similarity 28.4 es 137; Conservative
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                                                                                                                                                                                                                                                               WGLLLGGIIF---GUDEKSPPAMKTDVFFLYLLPPIVLDAGYFMPTRPFFENLGTIFWY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMTIRPLVDLLAVKKKQ------ETKRSINEEIHTQFLDH------LLTGIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARP 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETFI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ANYD-SIGISDIFLGFLSFFVVALGGVFVGVVYGVIAAFTSR---FTSHIRVIEPLFV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLLYAVCLVGGEQIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID
                                                                                                                 DETPLLYSLYFGEGVVNDATSVVLFNAIQSF----DMTSFDPKIGLHFIGNFLYLFLSST 225
                                                                                                                                                                                                                   GAIGTL----ISCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DICGHYGHHHWKDKLNRFNKKYVK 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIFLGYSTVAGSHQWNWTFV-----ISTLL--FCLIARVLGVLVLTWFIN---KFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLYVGMDALDIE---KWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLAKKNS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLYSYMAYLSAELFHLSGIMALIASGVVMRPYVEANISHKSHTTIKYFLKMWSSVSETLI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF 200
                                                                                                                                                                                                                                                                                                                                    16.8%; Suc. 28.4%; Pred 77;
                                                                                                                                                                                                                                                                                                                                           Score 466; DB 2; I
Pred. No. 2.1e-27;
7; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                      Length 698;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                 74;
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                                                                                                                                                                                                                                                                                                                                                 16;
                                                                     Qy
                                                                                                               В
                                  日
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Qy Db	286 SHYTMHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVA :         :         :
Qy Db	y 343 VSSILVGLILVGRAAFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYN 402 
Qy	403 K
Дb	b 333LLPATVFPRKKLFITAAIVVIFFTVFILGITIRPLVEFLDVKRSNKKQQAVSE 385
Qy	)y 463 PSSPKHFTVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWRKEDDSF 518
DЬ	386 EIHWCRFFDHVKTGIEDVCGHWGHNEWRDKFKKFDDKY 423
Qy	y 519 mr 520
Db	b 424 LR 425
ប្បធ្¥ង្	RESULT 13  A48858  Na+/H+-exchanging protein - pig (C;Species: Sus scrofa domestica (domestic pig) C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000 C;Date: 19-Dec: A48858: 146613
> > > 2 Z X (	R;Reilly, R.F.; Hildebrandt, F.; Biemesderfer, D.; Sardet, C.; Pouyssegur, J.; Am. J. Physiol. 261, F1088-F1094, 1991 Am. J. Physiol. 261, F1088-F1094, 1991 A;Title: cDNA cloning and immunolocalization of a Na(+)-H+ exchanger in LLC-PK1 A;Reference number: A48858; MUID:92087905 A:Accession: A48858
*****	A; Status: preliminary A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-818 <rei> A; Residues: 1-818 <rei> A; Cross-references: GB:S71135; NID:g240706; PIDN:AAB20633.1; PID:g240707 A; Cross-references: LLC-PKI kidney cell line A; Experimental source: LLC-PKI kidney cell line A; Experimental source: LLC-PKI kidney cell line</rei></rei>
* # # # # #	R;Reilly, R.F.  Am. J. Physiol. 261, 1088-1094, 1991  A;Title: cDNA cloning and immunolocalization of a Na+-H+ exchanger in LLC-PK1  A;Referen number: I46613
A A A ;	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-682,'H',684-818 <re2> A;Cross-references: GB:M89631; NID:g164595; PIDN:AAA31092.1; PID:g164596</re2>
	Query Match 16.6%; Score 460.5; DB 2; Length 818; Best Local Similarity 28.0%; Pred. No. 6.5e-27; Matches 145; Conservative 108; Mismatches 181; Indels 83; Gaps
9 0	Qy 25 MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL 83 :: :: :
9 0	QY 84 FEIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGAVKIFKHLDID 141
D D	QY 142 FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF 200
ם ס	Qy 201 DMTSEDPKIGLHEIGNELYLELSSTELGVGIGLLCAYIIKKLYEGRHSTDREVAL 255 bb 281ANYD-RVGIVDIVLGEL-SEFVVSLGGVFVGVVYGVIAAFTSRFTSHIRVIEPLE 333

256 MMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETF 315 : | ||::|: ||:|: | ::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::

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Montrose, M.H.;

Potter

rabbit ileal villus

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RESULT 14
A40204
A40204
Na+/H+-exchanging protein 1 - rat
N; Alternate names: Na+/H+ antiporter
C; Species: Rattus norvegicus (Norway rat)
C; Date: 28-Aug-1992 #sequence_revision 28-Aug-1992
C; Accession: A40204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Orlowski, J.; Kandasamy, R.A.; Shull, G.E. J. Biol. Chem. 267, 9331-933, 1992
A;Title: Molecular cloning of putative members rally related proteins.
A;Reference number: A40204; MUID:92250539
A;Accession: A40204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-820 <ORL>
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                                                                                                                                                                                                                                                                                                       GLSVAVSSILVGLILVGRAAFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLH--FIG--NFLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLGTILIFAVVGTLWNAFFLGGLLYAVCLVGGEQINNIGLLDTLLFGSIISAVDPVAVLA
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                                                                                                     MTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWR----K
                                                                                                                                                                                                                                                                                                                                                               SGVVMRPYVEANISHKSHTTIKYFLKMWSSVSETLIFIFLGVSTVAGSHQWNWTFV----
                                                                                                                                                                                                                                                                                                                                                                                                               CGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIE----KWKFVKNSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLGGVFVGVVYGVIAAFTSR---FTSHIRVIEPLFVFLYSYMAYLSAELFHLSGIMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPESCLLIVVGLLVGG--LIKGVGETPPFL--QSDVFFLFLLPPIILDAGYFLPLRQFTE 188
                                                                                                                                                          SLGY--LLDKKHFPMCD--LFLTAIITVIFFTVFVQGMTIRPLVDLLAVKKKQ---
                                                                                                                                                                                                            ALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSS
                                                                                                                                                                                                                                                            ----ISTLL--FCLIARVLGVLVLTWFIN---KFRIVKLTPKDQFIIAYGGL-RGAIAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEFASYEY---VGISDIFLGFLSFFVV
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Pred. No. 7.1e-27;
98; Mismatches 180
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                                                             -----DICGHYGHHHWKDKLNR
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A;Residues: 1-241,'A',243-568,'E',570-816 <HIL>
A;Residues: 1-241,'A',243-568,'E',570-816 ; PIDN:CAA43721.1; PID
A;Cross-references: EMBL:X61504; NID:g1653; PIDN:CAA43721.1; PID
A;Note: the authors translated the codon CTG for residue 646 as C;Reywords: glycoprotein; transmembrane protein
F:16-35/Domain: transmembrane #status predicted <TM2>
F:108-127/Domain: transmembrane #status predicted <TM3>
F:108-149/Domain: transmembrane #status predicted <TM4>
F:155-174/Domain: transmembrane #status predicted <TM6>
F:192-211/Domain: transmembrane #status predicted <TM6>
F:295-315/Domain: transmembrane #status predicted <TM7>
F:339-357/Domain: transmembrane #status predicted <TM8>
F:411-430/Domain: transmembrane #status predicted <TM9>
F:481-500/Domain: transmembrane #status predicted <TM9>
F:75,370/Binding site: carbohydrate (Asn) (covalent) #status predicted <TM9>
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A; Residues: 472-816 <-KLT>
A; Cross-references: EMBL: X56536; NID: g1666; PIDN: CAA39881.1; PID: g1667
A; Cross-references: EMBL: X56536; NID: g1666; PIDN: CAA39881.1; PID: g1667
R; Hildebrandt, F.; Pizzonia, J.H.; Reilly, R.F.; Reboucas, N.A.; Sardet, C.; Pouysseg Blochim. Biophys. Acta 1129, 105-108, 1991
A; Title: Cloning, sequence, and tissue distribution of a rabbit renal Na(+)/H(+) exch A; Reference number: S30602; MUID: 92096447
A; Accession: S30602
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FEBS Lett. 279, 25-29, 1991
A;Title: Identification of the protein and
A;Reference number: S13926; MUID:91138752
A;Accession: S13926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Na+/H+-exchanging protein - rabbit
N;Alternate names: Na+/H+ antiporter: Na+/H+ exchanger; pH regulatory protein
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 **sequence_revision 30-Sep-1993 **text_change 01-Dec-2000
C;Accession: S16328; S13926; S30602
R;Tse, C.M.; Ma, A.I.; Yang, V.W.; Watson, A.J.M.; Levine, S.; Montrose, M.H.
EMBO J. 10, 1957-1967, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-816 <TSE>
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MLMSYLSYIMABLEYLSGILTVEFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETFI
                                                                             --ANYDHVGIVDIVLGFL-SFFVVALGGVFVGVVYGVIAAFTSR---FTAHIRVIEPLFV
                                                                                                                                                                                                            FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF
                                                                                                                                                                                                                                                                               FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLMYAVCLVGGEQIN
                                                                                                                                                                                                                                                                                                                                                                                 ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGGLIKGV-GEKPPFL---QSEV
                                                                                                                          DMTSFD----PKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVALM
                                                                                                                                                                            NIGLLDNLLFGSIISAVDPVAVLAVFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEF 280
                                                                                                                                                                                                                                                                                                                                 FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID 141
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YGC_ECOLI
NAH2_SCHPO
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		P07117 escherichia			P14544 leishmania		P36606 schizosacci		P38206 saccharomy	P50974 rhodobacte	P39830 escherichia

## ALIGNMENTS

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RESULT 1
NAH6_HUMAN
EMBL; D87/*..,
MIM; 300231; -..
InterPro; LPR000676; NaH_Exc...
Pfam; PF0099; Na_H_Exchanger; 1.
PRINTS; PR01084; NAHEXCHNGR.
"ransmembrane; Sodium transport; Transport; Sy
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SEQUENCE FROM N.A.
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MEDLINE-98175963; PubMed-9507001;
Numata M., Petrecca K., Lake N., Orlowski J.;
"Identification of a mitochondrial Na+/H+ exchanger.";
"atol. Chem. 273:6951-6959(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 3:321-329(1996).

1. FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS FOR NA+ AND K+
THE MITOCHONDRIAL INNER MEMBRANE. CONTRIBUTES TO ORGANELLAR
AND CALCIUM HOMEOSTASIS.

1. SUBCELLULAR LOCATION: Integral membrane protein. Mitochondri
TISSUES SPECIFICITY: UBIQUITOUS; BUT IS MOST ABUNDANT IN
MITOCHONDRION-RICH TISSUES SUCH AS BRAIN, SKELETAL MUSCLE, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Seki N., Ishikawa K.-i., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human gene: The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced the coding sequences of 80 new genes (KIAAO201-RIAAO280) deduced the coding sequences of 80 new genes (KIAAO201-RIAAO280) deduced the coding sequences of 80 new genes (KIAAO201-RIAAO280) deduced the coding sequences of 80 new genes (KIAAO201-RIAAO280) deduced the coding sequences of 80 new genes (KIAAO201-RIAAO280) deduced the coding sequences of 80 new genes (KIAAO201-RIAAO280) deduced the coding sequences of 80 new genes (KIAAO201-RIAAO280) deduced the coding sequences of 80 new genes (KIAAO201-RIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280) deduced the coding sequences of 80 new genes (KIAAO280
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium/hydrogen exchanger 6 (Na(+)/H(+) exchanger
SLC9A6 OR NHE6 OR KIAA0267.
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MEDLINE-97191544; PubMed-9039502;
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Best Local
                                                                                                               NAH2_YEAST
Q04121;
30-MAY-2000
30-MAY-2000
30-MAY-2000
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                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mitochondrial sodium/hydrogen exchanger (Mito
                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                          exchanger).
NHA2 OR NHX1 OR YDR456W OR D9461.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 119
                                       Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----: LSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMT
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                                                                                                                                                                                                                                                                                                                                    L-RGAMAFALAIR-----DTATYARQMMFSTTLLIVFFTVWVFGGGTTAMLSCL----
                                                                                                                                                                                                                                                                                                                                                  LMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGLMTKPLINLLLPPHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLSQDETPL-LYSLVFGEGVVNDATSVVLFNAI------QSFDMTSFDPKIGLHFI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILAYAFLGTAISCFVIGSIMYGCVTLMKVTGQLAGDFY-FTDCLLFGAIVSATDPVTVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIHVPSDVNNVTLSCEVQSSPTTLLVTFDPEVFFNILLPPIIFYAGYSLKRRHFFRNLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAEESHRQDSANLL---IFILLTLTITITIWLFKHRRARFLHETGLAMIYGLLVGLVLRY
                                                                                                                                                                                                                                  MWYNFDHNYLKPLLTHSG
                                                                                                                                                                                                                                                          YWRKFDDSFMRPVFGGRG
                                                                                                                                                                                                                                                                                                           QMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHR
                                                                                                                                                                                                                                                                                                                                                                                                             VKNSQGLSVAVSSILVG---LILVGRAAFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAG
                                                                                                                                                                                                                                                                                                                                                                                                                                      TGVVAVLECGITQAHYTYNNLSTESQHRTKQLFELLNFLAENFIFSYMGLTLFTFQNHVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --FLGIFSGSFAMGAATGVVTALVTKFTKL---REFQLLETGLFFLMSWSTFLLAEAWGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFHELQVDVELYALLFGESVLNDAVAIVLSSSIVAYQPAGDNSHTFDVTAMFKSIGI---
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                                                                                                                                                                     STANDARD;
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266
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                                       Saccharomycetaceae;
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                     DSDQEHLGVPENERRTT - - - - - KAESAWLFR
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                                       Saccharomyces
                                                                                                      (Mitochondrial
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                                                                                                       Na(+)/H(+)
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                                                                                                                                                                                                                                                                                     536
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Best Local 9
Matches 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-981/2903, turned MEDLINE-981/2903, turned M., Petrecca K., Lake N., Orlowski J.; Numata M., Petrecca K., Lake N., Orlowski J.; Petrecca K., Lake N., Orlowski J.; Diol. Chem. 273:6951-6959(1998).

-I- FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS F. FUNCTION: ELECTRONEUTRAL EXCHANGE. CONTRIBUTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H. Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., P. Roberts D., Schramm S., Schroeder M., Shogren T., Shroff Winant A., Yelton M., Botstein D., Davis R.W.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane,
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          286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S0002864; NHX1
                                                                                                                                                        FMTIMLEGAIGTLISCSIISFGAVKIFKHLDIDFLD--FGDYLAIGAIFAATDSVCTLQV
                                                                                                                                                                                                                                                                           LLQNSDLFTSDHASV----VSMN------LFVALLCACIVLG---HLLEEN-RWV
SHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSS
                                                  FLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVM
                                   LIGVLIGILVALLLKHTHIRRY-PQIESCLILLIAYESYFFSNGCHMSGIVSLLFCGITL
                                                                                      FNAYKVDPKLYTIIFGESLLNDAISIVMFETCQKFHGQPATFSSVFEGAGLFLMTFSVSL
                                                                                                                LSQDET-PLLYSLVFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSST
                                                                                                                                           MLSILIFAIPGTFISAVVIGI-ILYIWTFLGLESIDISFADAMSVGATLSATDPVTILSI
                                                                                                                                                                                              HETVLSIFYGMVIGLIIRMSPGHYIQDTVTFNSSYFFNVLLPPIILNSGYELNQVNFFNN
                                                                                                                                                                                                                       NESITALIIGLCTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVN
                                                                                                                                                                                                                                                LLPSPDLPGSDDPIAGDPDVDLNPVTEEMFSSWALFIMLLLLISALWSSYYLTQKRIRAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00999; Na_H_Exchanger;
S; PR01084; NAHEXCHNGR.
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                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000676;
                                                                                                                                                                                                                                                                                                                                                                                             86
118
154
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218
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259
307
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138
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197
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27.2%;
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                                                                                                                                                                                                                                                                                                     117;
                                                                                                                                                                                                                                                                                                                                                         WW.
                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                Score 568; DB 1;
Pred. No. 3.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.;
exchanger.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Symport; Mitochondrion
                                                                                                                                                                                                                                                                                                                               Length
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h C., Petel 1
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RESULT NAME OF STREET OF S
                                                                                                                                                                                                        Ghishan F.K., Knobel S.M., Summar M.;

"Molecular cloning, sequencing, chromosomal localization, and distribution of the human Na+/H+ exchanger (SLC9A2).";

Genomics 30:25-30(1995).

-I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GE BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT COLONIC SODIUM ABSORPTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dubois R., Ghishan F.K.;

"Molecular cloning, sequencing, tissue distribution, and functional expression of a Na+/H+ exchanger (NHE-2).";

Proc. Natl. Acad. Sci. U.S.A. 90:3938-3942(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang Z., Orlowski J., Shull G.E.;
"Primary structure and functional expression gastrointestinal isoform of the rat Na/H exch J. Biol. Chem. 268:11925-11928(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93248205; PubMed-7683411; Collins J.F., Honda T., Knobel S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *TRAIN-SPRAGUE-DAWLEY; TISSUE-Small intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P48763; Q16434; 
01-FEB-1996 (Rel. 33, Last sequence up 
16-OCT-2001 (Rel. 40, Last annotation 
Sodium/hydrogen exchanger 2 (Na(+)/H(-
SLC9A2 OR NHE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96129297; PubMed=8595899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93280160; PubMed-7685026; Wang Z., Orlowski J., Shull G.E.;
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SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) &
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PREDOMINANTLY IN SMALL INTESTINE, COLON,
STOMACH, WITH MUCH LOWER LEVELS IN SKELETAL MUSCLE, KIDNEY,
TESTIS, UTERUS, HEART, AND LUNG.
PTM: PHOSPHORYLATED (POSSIBLE).
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2 (Na(+)/H(+) exchanger
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EMBL; S81591;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
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SLFGICQIEAFGLSDITLL---QNLLFGSLISAVDPVAVLAVFENIHVNEQLYILVFGES
                   SIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ-DETPLLYSLVFGEG
                                                     GGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTL-----ISC
                                          GVDEKSPPAMKTDVFFLYLLPPIVLDAGYFMPTRPFFENLGTIFWYAVVGTLWNSIGIGL
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family; Phosphorylation; Alternative splicing.
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ipr000676; NaH_Exchngr.
iprochanger; 1.
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813 AA;
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CYTOPLASMIC (POTENTIAL).

E (M5) (POTENTYAT:
                                                                                                                                                                                                    LYQIRQR ->
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EXTRACELLULAR (POTENTIAL)
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F (M5A) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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B (M2) HYDROPHOBIC.
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A (M1) HYDROPHOBIC
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p50482;
p50482;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger
SLC9A2 OR NHE2.
                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 268:11917-11924(1993).

-i- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
                                                                                                 entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and expression of a rabbit cDNA encoding a serum-activated ethylisopropylamiloride-resistant epithelial Na+/H+ exchanger isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93280159; PubMed=7685025;
Tse C.-M., Levine S.A., Yun C.H., Montrose M.H., Little Pouyssegur J., Donowitz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-NEW ZEALANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAH2_RABIT
                   PRINTS;
                                                                EMBL; L13733; -; NOT_ANNOTATED_CDS
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SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF H
                                                                                                                                                                                                                                                                                                    COLONIC SODIUM ABSORPTION.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: HIGH LEVELS IN INTESTINE AND KIDNEY
                                                                                                                                                                                                                                   DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS
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                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTRHSFATLSFVAETFIFLYVGMDALDIE---KWKFVKNSQGLSVAVSSILVGLILVGRA
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                                 Pro; IPR000676; NaH_Exchngr.
PF00999; Na_H_Exchanger; 1.
                   PR01084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZEALAND WHITE;
Glycoprotein; Sodium transport; Transport; Symport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                    There are no restrictions ong as its content is in
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                                                                                                                                      Usage
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                                                                                                                                        commercial
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                                                                                                                                                                                                                       VVNDATSVVLENAIQSE - - - - DMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYII
                                                                                                                                                                                                                                                                                           GGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTL----ISC 124
                                                          IMITSTYTYVLFSTYVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDN
                                                                               AFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENA
                                                                                                                                                               R---FTHNIRVIEPLFVFLYSYLSYITAEMFHLSGIMAITACAMTMNKYVEENVSQKSYT
                                                                                                                                                                        KKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRV
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                                                                                                                                                                                                                                                                                                                          VFTLDYPHVQIPFEITLWILLASLAKIGFHLYHKLPTIVPESCLLIMVGLLLGGIIF---
VKTGIEDVC-
                    QPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWR----KFDDSFMR
                                                                                                                       TIKYFMKMLSSVSETLIFIFMGVSTVGKNHEWNWAFV-----
                                                                                                                                          TTRHSFATLSFVAETFIFLYVGMDALDIE---KWKFVKNSQGLSVAVSSILVGLILVGRA
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147; Conserv
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27.8%;
                                                                                                                                                                                                                                                                                                                                                                86; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Score 482.5;
Pred. No. 1.:
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E (M5) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
F (M5A) (POTENTIAL).
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C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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J (M8) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTEN
I (M7) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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G (M5B) (POTENTIAL).
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B (M2) (POTENTIAL)
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 -GHWGHNFWRDKFKKFDDKYLR
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                                        -DVKRSNKKQQAVSEEIHCRFF
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nes 216;
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                                                                                                                        -CFTLAFCLIWRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger
SLC9A2 OR NHE2.
                                                                                                    TRANSMEM
DOMAIN
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EMBL; AC007239; AAF19248.1;
MIM; 600530;
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-1- FUNCTION: INVOLVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UBY0;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99375108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mitted (APR-1999) to the EMBL/GenBank/DDBJ databases. FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLONIC SODIUM ABSORPTION.

SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE,
KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s:
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J. Physiol. 277:G383-G390(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTESTINE.
                                                                                                                                                                                                                                                                                                                                                                                             PR01084; NAHEXCHNGR.
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IPR000676; NaH_Exchngr.
" ""changer; 1.
                                                                                                                                                                                                                                                                                                                                                            family;
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dal R.Y., Schmidt
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100
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1168
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                                                                                                                CYTOPLASMIC (POTENTIAL).

B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
D (M4) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
E (M5) (POTENTIAL).
E (M5) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
F (M5A) (POTENTIAL).
F (M5A) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
G (M5B) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
H (M6) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
I (M7) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
A (M1) HYDROPHORIC
                                                                                                                                                                                                                                                                                                                                                                         Sodium transport; Transport;
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Catarrhini; Hominidae;
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DENOMINATION OF HYDROPHOBIC
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Best Local
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                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger
SLC9A1 OR NHE1.
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CARBOHYD
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TRANSMEM
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Q61165;
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DOMAIN
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DOMAIN
                                                                                                                                                                                                 MOUSE
                                                                         NCBI_TaxID=10090;
                                                                                     Mammalia; Eutheria;
                                                                                              Eukaryota; Metazoa;
                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                          -EIYCRLFDHVKTGIEDVC-----
                                                                                                                                                                                                                                                             KHFTVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWR----KFDDSFMR
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                                                                                                                                                                                                                                                                                                                                            EENVSQKSYTTIKYFMKMLSSVSETLIFIFMGVSTVGKNHEWNWAFV---
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812 AA;
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Rodentia;
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EXTRACELLULAR (I
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Pred.
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J (M8) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

K (M9) (POTENTIAL).
                                                                                   Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                     PRT;
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Dewey M.J., Bowman L.H.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL

GENERATED

STRAIN-BALB/C; SEQUENCE FROM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000676; NaH_Exchngr.
Pfam; PF00999; Na_H_Exchanger; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+)
CAUTION: THE NUMBER, LOCALIZATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSDUCTION.
                                                                                                                                                                                                                       MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the En
  DMTSFDPKIGLH--FIG--NFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGI:102462;
                                                                               FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF
                                                                                                                      FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLLYAVCLVGGEQIN
                                                                                                                                                           FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID 141
                                                                                                                                                                                                ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGG--LIKGVGETPPFL--QSDV
                                           NIGLLDTLLFGSIISAVDPVAVLAVFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEF
                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family;
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                                                                                                                                                                                                                                                                                                  17.1%;
28.4%;
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K (M9) (POTER
                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (P 0589C4D08DD348BE CRC64;
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C (M3) (POTENTIAL).
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J (M8) (POTENTIAL).
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CYTOPLASMIC (POTEN
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G (M5B) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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F (M5A) (POTENTIAL)
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E (M5) (POTENTIAL).
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B (M2) HYDROPHOBIC.
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                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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DENOMINATION OF HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                189;
                                                                                                                                                                                                                                                                                                                   Length 820;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                                                              71;
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RESULT 7
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01-AUG-1992
15-JUL-1999
                                                                                             entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                    Tse C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M.;
"Cloning and sequencing of a rabbit cDNA encoding an intestinal and
kidney-specific Na+/H+ exchanger isoform (NHE-3).";
J. Biol. Chem. 267:9340-9348(1992).

-i- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
THE ANGRESSIA.
                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-NEW ZEALAND WHITE; TISSUE-Ileal villus, and Kidney cortex; MEDLINE-92250540; PubMed-1374392; Tse C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; 
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLC9A3 OR NHE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sodium/hydrogen exchanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P26432;
                                             EMBL; M87007; AAA314
PIR; A40205; A40205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAH3_RABIT
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                                                                                                                                                                                                                       DESCENDING COLON.

PETM: PHOSPHORYLATED (POSSIBLE).

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC CAUTION: IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: INTESTINAL AND KIDNEY SPECIFIC. MOST ABUNDANT
IN KIDNEY CORTEX, FOLLOWED EQUALLY BY ILEUM AND ASCENDING COLON,
THEN KIDNEY MEDULLA AND JEJUNUM. IS ABSENT FROM DUODENUM AND
                                                                                                                                                                                                                                                                                                                                                                               TRANSDUCTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ASYD-SVGISDIFLGELSFEVVALGGVFVGVVYGVIAAFTSR---FTSHIRVIEPLEV
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                                                                                             s requires a license agreement (
an email to license@isb-sib.ch)
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                                                                AAA31420.1;
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38, Last annotation update)
changer 3 (Na(+)/H(+) exchanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lagomorpha;
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                                                                                                                                        There are no resung as its content
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InterPro; IPR000676; NaH\_Exchngr.
pfam; pF00999; Na\_H\_Exchanger; 1.
pRINTS; pR01084; NAHEXCHNGR.

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Query Match
Best Local S
Matches 148
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Multigene fami
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                                                                                                                                                                                                     LAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAY----NKFTTSGHTSLHENAIMITSTV : | | ::::|:
                                                      DISG
                                                                                                                                                                                   RYRMVQLELI----DQVVMSYGGL-RGAVAFALVALLDGNK-----VKEKNLFVSTTI
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                                                                                  MITGPEVARPTALRMLLRTPTHTVHRY - - - - WRKFDDSFM
                                                                                                                                                  TVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESD
                                                                                                                                                                                                                                                    SGAETIIFMFLGISAVDPLIWTW------NTAFVLLTLLFVSVFRAIGVVLQTWLLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMGELKIGLLDF----LLFGSLIAAVDPVAVLAVFEEVHVNEVLFIIVFGESLLNDAVTVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGAVKIF---
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                                                   -QIGHNYLRDKWANFDRRFL
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M8 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

M9 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

M10 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).

#5B (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

#6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

#7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 471.5;
Pred. No. 6.1
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M4 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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M2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
M3 (POTENTIAL).
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M1 (POTENTIAL)
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N-LINKED (GLCNAC .) (
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                                                                                                                  ·KVKRSEHREPKLNEKLHGRAFDHIL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                   514
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NAH3_RAT STAN
P26433;
O1-AUG-1992 (Rel. 2
O1-AUG-1992 (Rel. 2
15-JUL-1999 (Rel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           related proteins.";
J. Biol. Chem. 267:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sodium/hydrogen exchanger 3 (Na(+)/H(+) exchanger SLC9A3 OR NHE3.
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or send an
                          entities requires
                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family. cDNA cloning, deduced amino acid sequence, expression of the rat Na/H exchanger NHE-1 and two
                                                                                                                    between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92250539; PubMed-1577762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                            European
                                                                                                                                                                               PTM: PHOSPHORYLATED (POSSIBLE):
SIMILARITY: BELONGS TO THE MA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HY
DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral mer
TISSUE SPECIFICITY: MOST ABUNDANT
                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                              FOLLOWED BY KIDNEY AND STOMACH
                                                                                                                                                                                                                                                                                                                                                TRANSDUCTION.
                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                             non-profit institutions as long and this statement is not removed.
equires a license agreement (See http://www.isb-sib.email to license@isb-sib.ch).
                                                             Bioinformatics Institute. The profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Kidney;
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EMBL; M85300; AAA41702.1; -. PIR; B40204; B40204. interPro;

Symport;

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B (M2) HYDROPHOBIC.

CYTOPLASMIC (POTENTIAL).

C (M3) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

D (M4) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

E (M5) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

F (M5) (POTENTIAL). EXTRACELLULAR (POTENTIAL)
H (M6) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
I (M7) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
OTHER (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
K (M9) (POTENTIAL).
EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL).
G (M5B) (POTENTIAL). CYTOPLASMIC (POTENTIAL) Sodium transport; Transport; (M1) HYDROPHOBIC (POTENTIAL) (POTENTIAL)

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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Na(+)/H(+) exchanger beta (Na(+)/H(+) antiporter) (Bet
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
nichtschaft, Salmoniformes; Salmonidae; Oncor
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CARBOHYD
                                        Borgese F., Sardet C., Cappadoro M., Pouyssegur J., Motais R.; "Cloning and expression of a CAMP-activated Na+/H+ exchanger: evidence that the cytoplasmic domain mediates hormonal regulation."; Proc. Natl. Acad. Sci. U.S.A. 89:6765-6769(1992).
-!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
                                                                                                                                                                                                                                                                                                                                      ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                TISSUE=Nucleated erythrocyte;
MEDLINE=92357712; PubMed=1379718;
                                                                                                                                              SEQUENCE FROM N.A.
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                ACTIVE METABOLISM OR TO COUNTER NDITIONS. MAJOR PROTON EXTRUDING
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27.7%;
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EXTRACELLULAR (POTENTIAL).

M (M10) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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PTM: ACTIVATED BY CAMP, PROTEIN KINASE A AND PROTEIN KINASE C MISCELLANEOUS: INHIBITED BY AMILORIDE AND 5-AMINO-SUBSTITUTED DERIVATIVES AND ACTIVATED IN A COOPERATIVE FASHION BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. The by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a
                                         LPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLIS-----CSIISFGAVKIFKH
 LDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNA
                                                               LLALLMKLGFHLIPRLSAVVPESCLLIVVGLLVGGLIKVI--GEEPPVL--DSQLFFLCL
                     LPPIILDAGYFLPIRPFTENVGTILVFAVIGTLWNAFFMGGLLYALCQIESVG-----
                                                                                                      148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00999;
                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR01084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000676; NaH_Exchngr.
0999; Na_H_Exchanger; 1.
                                                                                                                                               759 AA;
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35
76
96
98
118
123
143
150
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA49549.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation
                                                                                                                                                                            85173
                                                                                                                16.9%;
                                                                                                     100;
                                                                                                                                               MW;
                                                                                                                                                                                                                            M8 (POTENTIAL).
CYTOPLASMIC (PO
                                                                                                                                                                                                                                                                     M6 (POTENTIAL).
CYTOPLASMIC (POM7 (POTENTIAL)
                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sodium transport; Transport;
                                                                                                                                             PHOSPHORYLATION (BY CAPK) (POTENTI PHOSPHORYLATION (BY CAPK) (POTENTIAL) N-LINKED (GLCNAC. . .) (POTENTIAL) N-LINKED (GLCNAC. . .) (POTENTIAL); D6D95442995AE251 CRC64;
                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL) M10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                      35
                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                               M5B (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
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                                                                                                                                                                                                                                         (POTENTIAL)
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                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                       184;
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                                                                                                                          Length 759;
                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Symport;
                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration
- outstation
                                                                                                       Gaps
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   196
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밁 ð В δÃ 밁 õ 밁 γO 밁

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EMBL; M85299; AAA98479.1; -.
PIR; A40204; A40204.
InterPro; IPR000676; NaH_Exchngr.
                                                                                                                                                                                                                                                                                                                                                                                                              Telated proteins.";

J. Biol. Chem. 267:9331-9339(1992).

I. FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY: TISSUE-Heart;
MEDLINE-9250539; PubMed-157762;
Orlowski J., Kandasamy R.A., Shuil G.E.;
"Molecular cloning of putative members of the Na/H exchanger gene family. cDNA cloning, deduced amino acid sequence, and mRNA tissue expression of the rat Na/H exchanger NHE-1 and two structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAH1_RAT
P26431;
Pfam; PF00999; Na_H_Exchanger; 1.
PRINTS; PR01084; NAHEXCHNGR.
Transmembrane; Glycoprotein; Sodium transport; Transport;
Multigene family; Phosphorylation.
DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger SLC9A1 OR NHE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              490
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                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: NOT TISSUE SPECIFIC.
PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                         DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS. CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARPTALRMLLRTPTHTVHRYWR----KEDDSEM-RPVEGGRGF 528
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                                                                                                                                               s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GVCGHYGHYHWKEKLNRFNKTYVKRWLIAGENF 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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Best Local
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                                                                                                                                                                                                        IVKLTPKDQFIIAYGGL-RGAIAFSLGY--LLDKKHFPMCD--LFLTAIITVIFFTVFVQ
                                                                                                                                                                                                                                                                                                                                                                                                  ASYEY---VGISDIFLGFLSFFVVSLGGVFVGVVYGVIAAFTSR---FTSHIRVIEPLFV
                                                                                                                                               GMTIRPLVDLLAVKKKQ
                                                                                                                                                                            GLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARP
                                                                                                                                                                                                                                          SDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVF
                                                                                                                                                                                                                                                                        FIFLGVSTVAGSHQWNWTFV-----ISTLL--FCLIARVLGVLVLTWFIN---KFR 444
                                                                                                                                                                                                                                                                                                      FLYVGMDALDIE----KWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSELSNLAKKNS
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820
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      STANDARD
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CYTOPLASMIC (POTENTIAL).
B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).

E (M5) (POTENTIAL).

EXTRACELULIAR (POTENTIAL).

F (M5A) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

G (M5B) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H (M6) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

I (M7) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

J (M8) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

K (M9) (POTENTIAL).
                                                                                                                KFDDSFMR
                                                                                                                                              ---ETKRSINEEIHTQFLDH--
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N-LINKED (GLCNAC. . .) (P
; 58398DE74A9642FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 467.5;
Pred. No. 1.
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EXTRACELLULAR (POTENTIAL)
D (M4) (POTENTIAL).
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     PRT;
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     822
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338

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DOMAIN
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P48761;
01-FEB-1996 (Rel. 33,
01-FEB-1996 (Rel. 33,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Sodium/hydrogen exchanger 1 (Na(+)/H(+) excha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Counillon L., Pouyssegur J.;
"Nucleotide sequence of the Chinese hamster Na+/H+ exchanger NHE1.";
Biochim. Blophys. Acta 1172:343-345(1993).
-!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRADING SYSTEM DRIVEN BY THE INWARD
SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
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                                                                                                                     DOMAIN
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                                    TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELULAR LOCATION: Integral membrane protein.

PTM: PHOSPHORYLAGED (POSSIBLE).

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSDUCTION.
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            WW;
 L, HYDROPHUBLC.

EXTRACELLULAR (POTENTIAL).

M (M10) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLONAC. . .) (POT
                                                                               J (M8) (POTE CYTOPLASMIC K (M9)
                                                                                                                                                                                                                              D (M4) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
E (M5) (POTENTIAL).
                                                                                                                                                                                                                                                                             B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
                                                                                                           EXTRACELLULAR (POTENTIAL)

J (M8) (POTENTIAL).
                                                                                                                                 H (M6) (POTENTIAL)
CYTOPLASMIC (POTEN
I (M7) (POTENTIAL)
                                                                                                                                                                              CYTOPLASMIC
G (M5B) (PO
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                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL) F (M5A) (POTENTIAL).
                                                                                                                                                                                                                                                               C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
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                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
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; Cricetinae;
            (POTENTIAL)
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Best Local S
Matches 144
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Q28362;
                          -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: PHOSPHORYLARED (POSSIBLE).
-!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
-!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                                 Amemiya M., Yamaji Y., Cano A., Moe O.W., Alpern R.J.;
"Acid incubation increases NHE-3 mRNA abundance in OKP cells.";
Am. J. Physiol. 269:C126-C133(199)
-i- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROFOR EXTRUDING SYSTEM DRIVEN BY THE INWARD
                                                                                                                                                                                                                                                                                    SLC9A3 OR NHE3.
Didelphis marsupialis virginiana (North American opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                               DIDMA
                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=95358256; PubMed=7631739;
                                                                                                                                                                                                                                                                                                                                                    Sodium/hydrogen exchanger
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                                                                                                        TRANSDUCTION.
                                                                                                                      SODIUM ION CHEMICAL GRADIENT. PLAYS
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 SWISS-PROT entry is copyright.
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(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 35, Created)
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Pred. No. 1.1e-
07; Mismatches
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use by non-profit institutions as long as its content is in
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Pfam; PF00999;
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                YRMVQLEIIDQVVMSYGGL-RGAVAYALV----VLLDEKKVKEKNLFVSTTIIVVFFTVI
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                                NSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTV
                                                                                    AETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLAKK
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                                                                       AETIIFMFLGISAVDPAIWTW--
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0999; Na_H_Exchanger; 1
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M10 (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC ) (POT
F6F9EF778D5DBBB2 CRC64;
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M5A (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
M5B (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
M6 (POTENTIAL).
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M1 (POTENTIAL).
EXTRACELLULAR (I
M2 (POTENTIAL).
CYTOPLASMIC (PO:
M3 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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M8 (POTENTIAL).
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Eukaryota; Metazoa;
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0999; Na_H_Exchanger; 1.
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CYTOPLASMIC (POTENTIAL)
E (M5)
                                                                            CYTOPLASMIC (POTENTIAL).
G (M5B) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                   B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
I (M7) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
J (M8) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                    H (M6) (POTENTIAL)
CYTOPLASMIC (POTEN
                                                                                                                                                                                                                                                                                             Sodium transport; Transport;
                                                                                                                     EXTRACELLULAR (POTENTIAL) F (M5A) (POTENTIAL).
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(POTENTIAL).

(POTENTIAL).

(POTENTIAL)

(POTENTIAL)

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TISSUE-Kidney cortex;
MEDLINE-95358265; PubMed-7631746;
Brant S.R., Yun C.H., Donowitz M., Tse
"Cloning, tissue distribution, and fun
Na+/N+ exchanger isoform, NHS3.";
Am. J. physiol. 269:C198-C206(1995).
entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Sodium/hydrogen exchanger 3 (Na(+)/H(+) exchanger 3) (NHE-3).
                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Electropean Bioinformatics Institute. There are no restricted the state of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrar PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+)
CAUTION: THE NUMBER, LOCALIZATION AND
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S. MAJOR PROTON EXYRUDING SYSTEM DRIVEN BY THE:
N CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN
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Primates; Catarrhini; Hominidae;
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LLC-PK1 renal Am. J. Physiol -1- FUNCTION:
                                                                     SEQUENCE FROM N.A.
MEDLINE=92087905; PubMed=
Reilly R.F., Hildebrandt
Pouyssegur J., Aronson P.
                                                                                                                                                                                                                                                               NAH1_PIG STANDARD; PRT; 818 AA. P48762; PFE-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger)
             MEDLINE=92087905; PubMed=1661081;
Reilly R.F., Hildebrandt F., Biemesderfer D., Sardet Reilly R.F., Hildebrandt F., Biemesderfer D., Sardet Pouyssegur J., Aronson P.S., Slayman C.W., Igarashi F. Pouyssegur J., Aronson P.S., Standard Indiana (1991) and Indiana (1991) and Indiana (1991).

**CDNA* cloning and immunolocalization of a Na(+)-H+ extra (1991) and Indiana (1991).

**Am. J. Physiol. 261:F1088-F1094(1991).
                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                             SLC9Al OR NHE1.
Sus scrofa (Pig).
                                                                                                                                                                    NCBI_TaxID=9823;
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                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92907
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EXTRACELLULAR (POTENTIAL).

M (M10) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLONAC. . .) (POTINICLULARC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 461; DB Pred. No. 2.8e 35; Mismatches
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REGULATION
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EXTRACELLULAR (POT
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2.8e-22;
TO
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                                     a Na(+)-H+ exchange
ELIMINATE ACIDS GENERATED
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                                                                                                                                                                                         Sus.
                                                                                                                                                                                                           Euteleostomi;
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                                                                                                                                                                                                                                                                     (NHE-1).
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Matches 145
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CONFLICT
SEQUENCE
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EMBL; S71135; AAB20633.1; -.
InterPro; IPR000676; NaH_Exchngr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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PTM: PHOSPHORYLARED (POSSIBLE).

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYI

DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN TRANSDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
NIGLLDNLLFGSIISAVDPVAVLAVFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEF
                                                                                                FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID
                                                                                                                                                  ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGGLIKAV--GETPPFL--QSEV
                                                                                                                                                                                         MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL
                               FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF
                                                                           FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLMYAVCLVGGEQIN
                                                                                                                                                                                                                               145;
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818
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28.0%;
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CYTOPLASMIC (POTENTIAL)
G (MSD)
                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).

J (M8) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

K (M9) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
D (M4) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                          M (M10) (POTENTIAL).
CYTOPLASMIC (POTENTI
N-LINKED (GLCNAC...
H -> Y (IN REF. 1; F
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                                                                                                                                                                                                                                                 Score 460.5; DB Pred. No. 3e-22;
                                                                                                                                                                                                                               Pred. No. 3e-
B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H (M6) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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F (M5A) (POTENTIAL)
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E (M5) (POTENTIAL)
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                   L, HYDROPHOBIC.

EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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DENOMINATION OF HYDROPHOBIC
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                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                 181;
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DC9 CRC64;
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collaboration -

European Bioinformatics Institute.

-!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
-!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

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RESULT 15

NAH1_RABIT
ID NAH1_
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DT 01-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and expression of a cDNA encoding the rabb villus cell basolateral membrane Na+/H+ exchanger."; EMBO J. 10:1957-1967(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P23791;
01-NOV-1991
01-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                               Hildebrandt F., Pizzonia J.H., Reilly R.F., Sardet C., Pouyssegur J., Slayman C.W., Aror "Cloning, sequence, and tissue distribution exchanger transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1). SLC9A1 OR NHE1.
                                                                                                                                                                                                                                exchanger."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Kidney;
MEDLINE=92096447; PubMed=1661611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RABIT
                                                                                                                                                                                                                                                        "Identification
                                                                                                                                                                                                                                                                                  Fliegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-NEW ZEALAND WHITE; TISSUE-Ileal villus; MEDLINE-91293066; PubMed-1712287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus
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01-NOV-1991 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                       MEDLINE-91138752; PubMed-1704856;
                                                                                                                                                                                                                                                                                                                                   STRAIN-NEW ZEALAND WHITE;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1129:105-108(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SUBCELLULAR LOCATION: Integral TISSUE SPECIFICITY: KIDNEY AND PTM: PHOSPHORYLATED (POSSIBLE)
                                                                                           3 LÉTT. 279:25-29(1991).
FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATI ETUNCTION: ENTABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                   TRANSDUCTION
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Chordata; Craniata; Vertebrata;
Chordata; Cranidae: Oryctola;
                                                                                                                                                                                                                                                     Sardet C., Pouyssegur J., Barr A.; tion of the protein and cDNA of the
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SEQUENCE
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EMBL; X61504; CAA43721.1; --
EMBL; X6536; CAA39881.1; --
PIR; S13926; S13926.
PIR; S16328; S16328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                 -- ANYDHYGIVDIVLGFL-SFFVVALGGVFVGVVYGVIAAFTSR--
               DMTSFD----PKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVALM
                                                                    FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLMYAVCLVGGEQIN
                                                                                     FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID 141
                                                                                                      ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGGLIKGV-GEKPPFL---QSEV 160
                                                                                                                         MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL 83
                                                                                                                                           144;
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                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-profit institutions as long
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0999; Na_H_Exchanger; 1.
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Pred. No. 3.
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N-LINKED (GLCNAC. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sodium transport; Transport;
                                                                                                                                                                                                                                                  M9 (POTENTIAL)
                                                                                                                                                                                                                                 M10 (POTENTIAL)
                                                                                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
M8 (POTENTIAL).
                                                                                                                                                                                                                                                                                              CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                       M5B (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                        M6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                         M5A (POTENTIAL
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-> E (IN REF. 2).
336738D267F7F436
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FTAHIRVIEPLFV
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Sean Job	DЬ	δÃ	B	Qy	Дb	Qy	ДĎ	Qy	DЪ	Qy
rch co time	536	494	496	434	441	374	395	317	335	257
Search completed: October 18, 2002, 12:26:10 Job time : 19 secs	536DICGHYGHHHWKDKLNRENKKYYK 559	494 TALRMLLRTPTHTVHRYWRKEDDSFMR 520	IHTQFLDH	434 GLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMTTGPEVARP 493	441 IVKLTPKDQFIIAYGGL-RGAIAFSLGYLLDKKHFPMCDLFLTAIITVIFFTVFVQ 495	SDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVF 433	395 FIFLGVSTVAGSHHWNWTEVISTLLFCLIARVLGVLGLTWFINKFR 440	317 FLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLAKKNS 373	335 FLYSYMAYLSAELFHLSGIMALIASGYVMRPYVEANISHKSHTTIKYFLKMWSSVSETLI 394	257 MLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETFI 316

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   Score
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

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2768
1 MAFGLSSLLQNSDLFTSDHA......FGGRGFVPFVAGSPVEQSPR
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   GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/1/1aa/BCTUS_COMB.pep:*
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US-08-114-070A-1
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US-09-087-332A-13
US-08-461-105-14
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US-08-961-116-15
US-09-144-914-8
US-08-986-768-2
US-09-097-889-15
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GENERAL INFORMATION:
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2 US-09-045-583-55 2 US-08-672-8140-2 4 US-09-333-696-2 2 US-08-225-480-7 2 US-08-928-692-58 2 US-08-995-522-4 2 US-08-995-522-4 3 US-08-965-522-4 3 US-08-965-6047-7 4 US-09-066-047-7 5 US-08-928-692-12 5 US-08-928-692-12 6 US-09-328-320-2 7 US-09-328-320-2 8 US-09-328-320-2 9 US-09-328-320-2
US-09-045-583-55 US-08-672-814D-2 US-09-333-96-2 US-09-333-996-7 US-09-097-758 US-08-928-692-4 US-08-96-522-4 US-08-96-522-4 US-08-96-522-1 US-09-066-047-7 US-09-086-545-2 US-09-328-320-2

## ALIGNMENTS

INFORMATION:

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TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 12

SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-734A-12
                    Query Match
Best Local
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brant, Steven R. APPLICANT: Yun, Chris C.H. APPLICANT: Donowitz, Mark APPLICANT: Tse, Chung-Ming TITLE OF INVENTION: Cloning, TITLE OF INVENTION: HE3.

NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIT: 20005-3315
ZIT: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FORG1s, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                                        TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 I St. CITY: Washington STATE: D.C.
    Local Similarity nes 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/677,734A FILING DATE: 10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Dunner
1300 I Street, N.W., Suite 700
    Conservative
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17.0%; Score 471.5;
28.4%; Pred. No. 3.66
ative 92; Mismatches
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                                                                                                                                                                                                                                                                                                 05387.0043-00000
                    .6e-38;
                                       DB 2;
                                       Length
  Indels
                                       832;
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Gaps
18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tse, Chung-Minc
TITLE OF INVENTION: Clonii
TITLE OF INVENTION: Funct:
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
             NAME: FORCIS, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396 RMVQLELI---DQVVMSYGGL-RGAVAFALVALLDGNK-----VKEKNLFVSTTIIV
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                                                                                                                                                                                                                                                                                    CITY: Washington
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                                                                                                           FILING DATE: 10-JUL-1996
                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
TELEPHONE:
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                                                                                                                                                                                                                                                       USA
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(202)
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                               05387.0043-00000
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                                                                                                                                                                                                                                                                                    Sequence 9, Application Patent No. 5871919
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                       APPLICANT: Tse, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Functional Analysis Of The Human
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
 COMPUTER READABLE FORM:
                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                479
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                                                               STREET:
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              COUNTRY: USA
ZIP: 20005-3315
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                                               STATE:
                                                                                           ADDRESSEE:
                                                                                                           ADDRESSEE:
                                                            Washington
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D.C

E: Dunner 1300 I Street,

N.W.,

Suite

Finnegan, Henderson, Farabow,

Garrett

Na+/H+ Exchanger Isoform

Yun, Chris C.H. Donowitz, Mark Brant, Steven R.

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RESULT 3
US-08-677-734A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 IIEPGFVFVISYLSYLTSEMLSLSAILAITFCGICCQKYVKANISEQSATTVRYTMKMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 IIALWILVASLAKIVFHLSH--KVTSVVPESALLIVLGLVLGGIV-----WAADHIASFT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 VVSMNLFVALLCACIV-LGHLLEENRWVNESITALIIGLCTGVVILLLSGGKSSHLLVF- 79
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                                                                                                                                                              DSESDMITGPEVARPTALRMLLRTPTHTVHRY----WRKFDDSFMRPV
                                                                                                                                                                                                                                                                                                 RMVQLETI----DQVVMSYGGL-RGAVAYALV----VLLDEKKVKEKNLFVSTTLIVVFFT
                                                                                                                                                                                                                                                                                                                                                                                                                    FVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLS
                                                                                                                                                                                                                                                    TVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPK-----HFTVPLLDNQP 478
                                                                                                                                                                                                                                                                                                                                                                                          SGAETIIFMFLGISAVDPVIWTW-----NTAFVLLTLVFISVYRAIGVVLQTWILNRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYNVFESFVTLGGDAVTGVDCVKGIVSFFVVSLGGTLVGVIFAFLLSLVTR---FTKHVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFNAIQSFDMTSFDPKIGLHF---IGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMGELKIGLLDF---LLFGSLIAAVDPVAVLAVFEEVHVNEVLFIIVFGESLLNDAVTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ-DETPLLYSLVFGEGVVNDATSVV
                                                                                                                                                                                                         VIFQGLTIKPLVQWL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTPTLFFFYLLPPIVLDAGYFMPNRLFFGNLGTILLYAVIGTIWNAATTGLSLYGVFLSG 166
                                                                                                                                                                                                                                                                                                                                             KKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFS
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27.7%;
US/08677734A
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                                                                                                                ----QIGHNYLRDKWSNFDRKFLSKV 515
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Pred. No. 7.2e-38;
                                                                                                                                                                                                         ·KVKRSEQREPKLNEKLHGRAFDHILSAIED - - -
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                                               Sequence 10, Application US/08677734A Patent No. 5871919
GENERAL INFORMATION:
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Best Local Similarity
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                APPLICANT:
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LENGTH: 834 amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: FORGIS, Jean B.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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   APPLICANT:
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                          HFDRKFLSRV
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                Brant, Steven R. Yun, Chris C.H.
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Donowitz, Mark
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Pred. No. 4e-37;
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Best Local S
Matches 140
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FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOIGLS, Jean B.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 VNESITALIIGLCTGVVILLLSGGKSSHLLVF--SEDLFFIYLLPPIIFNAGFQVKKKQF 105
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les 140; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                SMTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHRY----WR
                                                                    FALV----VLLDGDKVKEKNLFVSTTIIVVFFTVIFQGLTIKPLVQWL----KVKRSEHR
                                                                                                        IALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHS 456
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1300 I Street,
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-QIGHNYLRDKWS
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                                        Matches
                                                   Query Match
Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 60/000,788
FILING DATE: 03-JUL-1996
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                          NAME/KEY: Region LOCATION: 323..357 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                    NAME/KEY: Region
LOCATION: 115..144
OTHER INFORMATION: /
OTHER INFORMATION: 4
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LOCATION:
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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CLASSIFICATION: 435
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STATE: California
 56 IIGLCTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAG----FQVKKKQFFVNFMT 111
                                                                                                                 OTHER INFORMATION: OTHER INFORMATION:
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TYPE: amino acid
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Razan, J. Fernando
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McClanahan, Terrill K.
                                        Conservative
                                                                                                                                              Region 359..386
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US-09-213-053-2
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Best Local Similarity
Matches 114; Conserv
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LENGTH: 1394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS FILE REFERENCE: 454313-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/213,053
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 9608242
EARLIER FILING DATE: 1996-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: AUDONNET, Jean-Christophe APPLICANT: BAUDU, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: PCT/FR97/01115
EARLIER FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                        IISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEGV- 184
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-AIKIILILSLSFL--
                                                                                                                                                                                                                                   4.0%; Score 109.5; DB 4; ilarity 20.4%; Pred. No. 0.087; Conservative 84; Mismatches 195;
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    -----TICTIKI----HIFYLISILNGSGSH 577
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US-09-014-969-11
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                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PLEASE #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                NAME: Sprunger, Suza
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 02140
TOPOLOGY: 11
                                   TYPE: amino acid
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LaVallie, Edward R.
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linear
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                                                                                                                                                                Suzanne A.
BER: 41,323
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RESULT 8
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                                                                                                                                                                                                                                                                                                        Patent No. 5834237
GENERAL INFORMATION:
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Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                      Sequence 1,
                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                     487
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                                                                                                  CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 IQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGV-----GIGLLCAYIIKKLYFGRHSTD
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                                                                                                                                                                    STREET:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
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                                                                                                                                                                                                                                                                                                                           , Application US/08714070A 5834237
                                                                                                                                                                    E: BURNS, DOA
P.O. Box 1404
                                                                                                                                                                                                                                                            JACOBS, Eric
SILVESTRE, Nath
SCHWEINBRYBER,
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US/08/714,070A
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                              Version
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CITY:

New York

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RESULT 9
US-08-928-692-13
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Sequence 13, Application US/08928692 Patent No. 5958727
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                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 017753-077
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: 7703 826-6620
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APPLICATION NUMBER: FR 94/01767
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                            DSLYWNPSPSFESQVNSVRRIYARLELWKSDLHSSVVFDESAVQHPLFRSNAHVQMIYDN
                                                                                                                                                                                                                                                                                                                                                                                           DKI-----SFRQQI-----IIWWAGLMRGAV--SIALAYNKFTTSGHTS-LHEN 415
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Lamsa, Michael
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19.9%;
                                                                                        Methods for Modifying the Production
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                         5958727disk of No.
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                         5958727th America, Inc.
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RESULT 10
US-08-466-343D-2
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                                  Sequence 2, Application Patent No. 6025154
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.6%; Score 99; DB 2; Length 584; Best Local Similarity 18.7%; Pred. No. 0.26; Matches 89; Conservative 70; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
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APPLICANT: LI, YI TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                              SFATLSFVAETFIFLYVGMD---ALDIEK-----
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                                                                                                                                                                                                                                                                                                                                                  ---WKFVKNSQGLSVAVSSILVGLILVGRAAFV-----FPLSFLSNLAKKNSS----
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POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
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US-09-087-232A-13
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                                                                                      Sequence 13, Application US/09087232A Patent No. 6153431
GENERAL INFORMATION:
APPLICANT: Quillent et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LEGGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                   APPLICANT: Quillent et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 371-2600
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES:
                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                 307
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                                                                                                                                                                                                                                                                                                  250 ---PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRN 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
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     ADDRESSEE:
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                                                                                                                                                                                                                               YLL 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 3.5%; Score 97.5; DB 3; Similarity 21.8%; Pred. No. 0.17; 66; Conservative 53; Mismatches 127;
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 Baker & Botts, L.L.P. attn. Lisa Kole
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                                                                                                                                        Sequence 14, Application US/08861105 Patent No. 6258527
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                                                GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
APPLICANT: DENG, HONGKUI
APPLICANT: ELLMEIER, WILFRIED
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
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TELEFAX: (212) 765-251
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 28 MAY 19
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APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                           173 PLLYSLVFGEGVV-NDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGI 231
                                                                                                                                                                                                                                    278 VFFCGIVMSHYTWHNVTESSR---VTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVK 334
                                                                                                                                                                                                                                                                                                                                 232 GLLCAY------IIKKLYF-GRHSTDREVALMMLMSYLSYIMAELFYLSGILT 277
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                                                                                                                                                                                                                                                                                  84 PFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHA-VFALKARTV
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                                                                                                                     NSQGLSVAVSSILVGLI--LVGRAAFVFPLSFLSNLAKKNSSDKISFRQQII--IWWAGL 390
---PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRN
                                                                                                                                                                                       TF--GVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSH-FPY-----SQYQFWK
                                              MRGAVSIALAYNKF-----TTSGHTSLHENAIMITST--VTVVLFSTVVFGLMTKPLIN 442
                                                                                             NFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA--
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30 MAY 1997
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Pred. No. 0.17;
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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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INFORMATION FOR SEQ ID NO: 14:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
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ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
CITY: Hackensack
STATE: New Jersey
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LENGTH: 352 amino acids
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APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
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CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
CLASSIFICATION: 436
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    143 TF--GVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSH-FPY------SQYQFWK 191
                                                                                                                                                                   192 NFQTLKIVILGIVLPLLYMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA-- 249
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307 YLL 309
                                      443 LLL 445
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                                                                                250 ---PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRN
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RESULT 14

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RESULT 15
US-09-268-140-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617)227-7
TELEFAX: (617)742-421
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: FRAGMENT TYPE:
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TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled NUMBER OF SEQUENCES: 56
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LENGTH: 352 amino acids
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OPERATING SYSTEM:
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ilarity 21.8%;
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.17;
53; Mismatches 127
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Best Local :
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APPLICANT: Drabkin, Harry A.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED TITLE REFERENCE: 93445-00004
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SOFTWARE: Patentin V
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                                           371 KNSSDKISFRQQIIIWWAGLMRGAVSI--------ALAYNKFTTS 407
                                                                                     456 KLDDYVYYVRSTG---SIIEFIFGVVMFGNGAYTMMFESGSKIRAFMMCLHAYFNIYLQA 512
                                                                                                                              326 DIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLS----
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WKTFMNRRTAVKKINSLPEIKGSRLQEINDVCAICYHEFTTS
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Search completed: October 18, 2002, 12:24:38 Job time: 19 secs

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Result
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is derived by analysis of the total score distribution.
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## ALIGNMENTS

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RESULY 1

OPFEB3;

DP G1+MAR-2001 (TTEMBLIVEL. 16, Last sequence update)
DT 01+MAR-2001 (TTEMBLIVEL. 19, Last annotation update)
DC N+HILL EXCHANGER PROTEIN).

OC Pharbitis nl. (Violet) (Japanese morning glory).

OC Eukaryota; Viridiplantae; Streptophyta; Eubryophyta; Eubryophyta; Eudlicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.

ON NCBI_TaxID=35883;

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RR SEQUENCE FROM N.A.

RR SEQUENCE FROM N.A.

RC STRAIN-FR-R; TISSUE-LEAF;
RX MEDLINE-212/6661; PubMed=11382810;
RA Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Saito N., Iida S.;
RT Genes Encoding the Vaccolar Na+/H+ Exchanger and Flower Coloration.";
RA Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Kusumi T., Iida S.;
RT Genes Encoding the Vaccolar Na+/H+ Exchanger and Flower Coloration.";
RA Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Kusumi T., Iida S.;
RT Genes Encoding the Vaccolar Na+/H+ Exchanger and Flower Coloration.";
RR PABLI, ABO3399; BABIG380.1; -
DR EMBL, ABO35062; BAB60899.1; -
DR EMBL, ABO35063; BAB60899.1; -
DR EMBL, ABO35063; BAB60899.1; -
DR EMBL, ABO35063; BAB60899.1; -
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01-DEC-2001 (Tremi
NA+/H+ EXCHANGER.
ITNHX1.
                                                                                           SEQUENCE FROM N.A.

MEDLINB=21276661; PubMed=11382810;

MEDLINB=21276661; PubMed=11382810;

Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Saito N.,

Yonekura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.,

Yonekura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.,

"Genes Encoding the Vacuolar Na+/H+ Exchanger and Floward Toward 
                                                                                                                                                                                                                                                                                            Ipomoea tricolor (Morning glory).

Bukaryota; Viridiplantae; Streptlophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
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NA/H ANTIPORTER NHX1.
                                                                                                                                                                                                                                                         MEDLINE=21330247; Polymenda A., Shono M., Hayakawa T.
                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                   AGNHX1.
Atriplex gmelini.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyllidae; Caryophyllales; Chenopodiaceae; Atriplex.
                                                          PRINTS; PRO1084; NAHEXCHNGR.
PROSITE; PS00453; FKBP_PPIASE_1;
SEQUENCE 555 AA; 61504 MW; A(
                                                                                                                                                                                            halophyte Atriplex gmelini.";
Plant Mol. Biol. 46:35-42(2001).
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Submitted (NOV-2000) to the
EMBL; AB051818; BAB56106.1;
SEQUENCE 553 AA; 61119 M
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Nierembergia.
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Best Local S
Matches 412
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01-DEC-2001 (Trem
01-DEC-2001 (Trem
01-DEC-2001 (Trem
NA H-ANTIPORTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;

"Plant Na-H antiportor.";

Submitted (NOY-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AB051817; BAB56105.1; -.

SEQUENCE 540 AA; 59510 MW; BCE2740F275E896A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petunia hybrida (Petunia).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

NCBI_TaxID-4102;
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                                                                                                                                                                                CTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKOFFVNFMTIMLFGAIG
                                                                    TLISFIIISLGAIGIFKKMNIGSLEIGDYLAIGAIFSATDSVCTLQVLNQDETPLLYSLV
                                                                                                                                                           CTGIVILLISGGKNSHILVFSEDLFFIYLLPPIIFNAGFQVKKKSFFRNFSTIMLFGALG
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Pred. No. 5.2e
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Matches 407
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01-JUN-2001 (TremBlrel. 17
01-DEC-2001 (TremBlrel. 19
01-DEC-2001 (TremBlrel. 19
SODIUM/PROTON EXCHANGER.
                                                                                                                                                                                                                       exchanger gene in grapefruit peel tissue.";
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY028416; AAK27314.2;
SEQUENCE 542 AA; 59836 MW: 1x07777
                                                                                                                                                                                                                                                                                                              Citrus paradisi (Grapefruit).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
enrosids II; Sapindales; Rutaceae; Citrus.
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NCBI_TaxID=37656;
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TFATLSFVAEIFTFLYVGMDALDIEKWRFVKGSPGTSVAASAMLMGLIMAGRAAFVFPLS
          SFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLS
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                                FGRHSTDREVAIMVLMAYLSYMLAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTKH
                                        FGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRH
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75.4%;
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Last sequence update)
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Pred. No. 1.8e-151;
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
NA+/H+ ANTIPORTER.
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"Na+/H+ antiporter in Suaeda salsa.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF370358; AAK53432.1;
SEQUENCE 556 AA; 61672 MW; DDF6AB696647D48E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suaeda maritima subsp. salsa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Suaeda.
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                                                                                                                                                                                                                                                                                                                  AIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVAL
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-VARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
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LTKPLILFMLPQPKHFT---
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                                                                  SASTVSDLGSPKSFSLPLLEDRQDSEADLGNDDEEAYPRG
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3; Mismatches
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Pred. No. 1
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1.4e-150;
nes 62;
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Matches 401
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Q9SXJ8;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
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Eukaryota; Viridiplantae; Strv
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzaae; Oryza
NCBI_TaxID-4530;
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Pfam; PF00999; Na_H_Exchanger; 1.
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MEDLINE=99326147; PubMed=10395929;
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                                LRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
                                                                            MTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARPTA
                                                                                                            KISFRQOIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGL 435
||::|||::|||:|||||||:||:||:
KITWRQQVVIWWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMITSTITVVLFSTMVFGM 435
                                                                                                                                                              LFLYVGMDALDIEKWEFASDRPGKSIGISSILLGLVLIGRAAFVFPLSFLSNLTKKAPNE
                                                                                                                                                                          IFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLAKKNSSD
                                                                                                                                                                                                                          MMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETF 315
                                                                                                                                                                                                                                                                          AIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVAL
                                                                                                                                                                                                                                                                                                            SRMNIGTLDVGDFLAIGAIFSATDSVCTLQVLNQDETPFLYSLVFGEGVVNDATSIVLFN
                                                                                                                                                                                                                                                                                                                         KHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEGVVNDATSVVLFN 195
                                                                                                                                                                                                                                                                                                                                                                         LLVFSEDLFEIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGAVKIF 135
                 LRMLLTKPTHTVHYYWRKFDDALMRPMFGGRGFVPFSPGSPTEQS
                                                                     MTKPLIRLLLP----
                                                                                                                                                                                                              MMLMAYLSYMLAELLDLSGILTVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFIAETF
                                                                                                                                                                                                                                                             ALQNFDLVHIDAAVVLKELGNFFYLFLSSTFLGVFAGLLSAYIIKKLYIGRHSTDREVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                401;
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AB021878; BAA83337.1; -.
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/ta; Liliopsida; Poales; Poaceae;
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Pred.
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RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottler P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottler P.,
RA Wincker P., Cattollco L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattollco L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattollco L., Weissenbach J., Saurin W., Quetier F.,
RA Winchefer M., Muller S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent D.,
RA Rooney T., Raudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L., Jenskins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Pai G., Militecher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Miltecher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
Thaliana, ", Sellers of chromosome 3 of the plant Arabidopsis
RT Tulainan, ", Sellers of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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EMBL; AC009465; AA651408.1; ...
InterPro; IPR001179; FKBP_PPlase.
InterPro; IPR000676; NaH_Exchanger; 1.
Pfam; PF00999; Na_H_Exchanger; 1.
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Q9CAW6;
Q1-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AIQSEDMTSEDPKIGLHEIGNELYLFLSSTELGVGIGLLCAYIIKKLYEGRHSTDREVAL
                                                                                                                                 KKLDIGTFDLGDFLAIGAIFAATDSVCTLQVLNQDETPLLYSLVFGEGVVNDATSVVLFN
                                                                                                                                                                   KHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEGVVNDATSVVLFN
                                                                                                                                                                                                                                                            LLVESEDLEFIYLLPPIIFNAGFQVKKKQFFRNFVTIMAFGAIGTVVSCTIISLGAIQFF
                                                                                                                                                                                                                                                                                           LLVFSEDLFFIYLLPPIIFNAGFQVKKKOFFVNFMTIMLFGAIGTLISCSIISFGAVKIF
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;; PS00453; FKBP_PPIASE_1;
E 546 AA; 60522 MW; BE
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BEA270D40446360B CRC64;
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01-MAY-1999 (T
01-JUN-2001 (T
SODIUM PROTON
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STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
MEDLINE-99145575; PubMed-9990049;
MEDLINE-99145575; PubMed-9990049;
Gaxiola R.A., Rao R., Sherman A., Grisafi P., Alper S.L.,
"The Arabidopsis thaliana proton transporters, AtNhxl and
"The Arabidopsis thaliana proton in yeast.";
function in cation detoxification in yeast.";
function in cation detoxification in yeast.";
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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PRINTS; PR01084; NAHEXCHNGR.
PROSITE; PS00453; FKB_PPIASE_1; UNKNOWN_1.
NON TEPP
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InterPro; IPR000676; NaH_Exchngr.
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putative Na+/H+ antiporter.";
e EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrE
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Torenia hybrida.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Spermatophyta; Magnoliophyta; Lamiales incertae sedis; Toreni Asteridae; euasterids I; Lamiales; Lamiales incertae sedis; Toreni
                                                                                                                                                                                                     SEQUENCE FROM N.A.

Tida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;

"Plant Na-H antiportor.";

Plant Na-H antiportor.";

Submitted (NOY-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AB051819; BAB56107.1; -.

SEQUENCE 555 AA; 61315 MW; FEF9556E029B3983 CRC64;
                                                                                                                                                                                                                                                                                                                                       THPURPLE.
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           VEGEGVVNDATSVVLENAIQSEDMTSEDPKIGLHEIGNELYLELSSTELGVGIGLLCAYI 238
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Bk
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F24P17 gen
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ datab:
EMBL; AC011623; AAF089577.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001179; FKBP_PPIAse.
InterPro; IPR000676; NaH_Exchangr.
Pfam; PF00999; NaH_Exchanger; 1.
PRINTS; PR01084; NAHEXCHARR.
PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SEQUENCE 552 AA; 61135 MW; FB4317D8A874FCE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
EukaryOta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosiderosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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(Tremblrel. 19, Last senotation update)
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Q94BM4;
01-DEC-2001 (TremB)
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NA+/H+ ANTIPORTER.
                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY040245; AAK76737.1; -. SEQUENCE 546 AA; 59704 MW; 45ElBCAB73E295C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rriticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Wang Z., Zhang J., Chen S.;
"Isolation and characterization of two Na+/H+ antiport
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                                                                                                                                                            FGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYII
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Q93YH2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
NA+/H+ ANTIPORTER, ISOFORM 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Venema K., Belver A., Donaire J.;
"Cloning and characterization of two
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SILSDGDQVSVDSITLFVALLCGCIVIGHLLEESRWINDSITTLVIGLSTGGIILLTTKG
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                                                                                             VLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDR
                                                                                                                  EVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFV
                                                                                                                                                                                    VLFNAIQKLDLSHINSRAALVFTGNFLYLFLASTFLGVLIGLLSAYLIKKIYLGRHSTDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1819.5; DB
Pred. No. 2.8e-13
6; Mismatches 8
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Best Local
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STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
The sequence of A. thaliana TM021B04.";
The sequence of A. thaliana TM021B04.";
The sequence of A. thaliana TM021B04.";
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01-DEC-2001 (TrEMBLrel.
A_TM021B04.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                           VILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLIS 123
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 GLLCAYIIKKLYFG--
                    TILLISKGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFRNFVTIMLFGAVGTIIS
                                                                                                                                                                                                                        Litted (JUN-1997) to the EMBL/GenBank/DDBJ
AF007271; AAB61069.1; -.
Pro; IPR001179; FKBP_PPTASE.
Pro; IPR000676; NaH_Exchangr.
PF00999; Na_H_Exchanger; 1.
PF00999; Na_H_EXCHANGER; UNKNOWN_1.
PF00999; Na_H_EXCHANGER; OAF2F235F1A258E
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ed (JUN-1997) to
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the EMBL/GenBank/DDBJ
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Last sequence update)
Last annotation updat
  RHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGI
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Pred. No. 1.1e
44; Mismatches
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edons; core eudicots; Rosid
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